4862 AGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACTCTECTACTCTTTER 1600/290

4893 BGL2.

ProLeuAspLeuProProIleIleGlnArgLeuHisGlyLeuSerAlaPheSerLeuHis 4922 CCACTGGATCTACCTCCAATCATCTAAAGACTCCCATGGCCTCAGCGCATTTTCACTCCAC GGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGTGAAAGTGAGGTG

4954 NCOI.

SerTyrSerProGlyGluIleAsnArgValAlaAlaCysLeuArgLysLeuGlyValPro 4982 AGTTACTCTCCAGGTGAAATCAATAGGGTGGCCGCATGCCTCAGAAAACTTGGGGTACCG TCAATGAGAGGTCCACTTTAGTTATCCCACCGGGGTACGGAGTCTTTTGAACCCCATGGC

5015 SPHI, 5035 KPNI,

ProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGly
5042 CCCTTGCGAGCTTGGAGACACCGGGCCCGGAGCGTCCGCGCTAGGCTTCTGGCCAGAGGA
GGGAACCCTCGAACCTCTGTGGCCCGGGCCTCGCAGGCGGATCCGAAGCCGTTTCT

5064 APAI, 5091 BALI,

GJYArgAlaAlaIleCysGlYLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLys
5102 GGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGCAGTAAGAACAAGCTCAAA
CCGTCCCGACGGTATACACCGTTCATGGAGAAGTTGACCCGTCATTCTTGTTTCCAGTT

5113 NDEI,

5174 NOTI, 5175 EAG1 XMA3, 5182 BALI, 5186 PVU2,

SerGlyGlyAsp1leTyrHisSerValSerHisAlAArgProArgTrpIleTrpPheCys
5222 AGCGGGGGAGACATTTATCACAGCGTGTCTCATGCCCGGCCCCGTGGATCTGTTTTGC
TCGCCCCCTTGTAAATAGTGTGCACAGAGTACGGGCGGGGGACCTAGACCAAAAGG

5240 DRA3,

LeuleuleuleuAlaAlaGlyValGlyIleTyrLeuleuProAsnArgMetSerThrAsn 5282 CTACTCCTGCTGCAGGGGTAGGCATCTACCTCCTCCCCAACCGAATGAGCACGAAT GATGAGGACGAACGACCTCCCCATAGATGGAGGAGGGTTGGCTTACTCGTTCCTTA

5295 PSTI,

ProlysfroGlnArgLysThrLysArgAsnThrAsnArgArgfroGlnAspValLysPhe CCTAAACCTCAAAGAACAACCAAACGTAACACCAACCGGCGGCCGCCGCAGACCAACTCAAGTC GGATTTGGAGTTTCTTGTGTTTGCATTGTGGTTGGCCCCGGGGTCCTGCAGTTCAAG

5380 NOTI, 5381 EAG1 XMA3, 5390 AAT2, 5401 SMAI XMAI.

ProGlyGlyGlyGlnIleValGlyGlyValTyrLeuLeuProArgArgGlyProArgLeu CCGGGTGGGGGTCAGATCGTTGGTGGAGTTTACTTTGTTGCCGCGCAGGGGCCCTAGATTG GGCCCACCGCCAGTCTAGCAACCACCTCAAATGAACAACGGGGGTCCCCGGGGATCTAAC GluGluAlaTleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaTleLysSer GAGGAGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCCGCGTGGCCATCAAGCC CTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCGGGCCACCGGTAGTTCAGG

4301 BGLI, 4308 BALI,

LeuthrGluArgLeutyrValGlyGlyProLeuthrAsnSerArgGlyGluAsnCysGly
4322 CTCACCGAAGGCTTTATGTTGGGGCCCTCTTACCAATTCAAGGGGGGGAGAATTGGGGC
GAGTGGCTCTCCGAAATACAACCCCGGGAGAATTGTTAAGTTCCCCCTCTTGACGCCG

4345 APAI.

- TyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCys
  4382 TATCGCAGGTGCCGCGGAGCGGCCTACTGACAACTAGCTGTGGAAAACCCCTCACTTGC
  ATAGGGTCCACGGGGGCGCTGGCCATGACTGTTGATCGACACCATTGTGGGAGTGAAC
- TyrllelyshlahrgalaAlacyshrgAlaAlaGlyLeuGlnAspcysthrMetLeuVal 4442 TACATCAAGGCCCGGCAGCCTGTCGAGCCGCAGGGCTCCAGGACTGCACCATGCTCGTG ATGTAGTTCCGGGCCCGTCGGACAGCTCGGGTCCCGAGGTCCTGACGTGGTACGAGCAC

4452 SMAI XMAI,

CysGlyAspAspLeuValValIleCysGluSerAlaGlyValGlnGluAspAlaAlaSer
4502 TGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGGCGAGC
ACACGCTGCTGAATCACAATAGACACTTTCGCGCCCCCAGGTCCTCCCCCCCTG

4508 DRD1, 4511 TTH3I,

- ProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAlaHisAsp 4622 CCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTCAGTCGCCCACGAC GGTCTTATGCTGGACCTCGAGTATTGTAGTACGAGGAGGTGCACAGTCAGCGGGTGCTG

4637 SACI.

GIYAlaGIyIyskrgValTyrTyrLeuThrArgAspProThrThrProLeuAlaArgAla GGGCGTGGAAAGAGGGTCTACTACCTCACCGTGACCCTACAACCCCCCTCGGAAGCT CGCGCACCTTTCTCCCAGATGATGAGTGGGCACTGGGATGTTGGGGGAACCCTCTCGA

4731 NRUI.

- AlatrpGluThrAlaArgHisThrProValAsnSerTtpLeuGlyAsnIleIleMetPhe
  4742 GCGTGGGAGACAGCAAGACACACTCCAGTCAATTCCTGGCTAGGCAACATAATCATGTTT
  CGCACCCTCTGTGTGTGTGAGGTCAGTTAAGGACCGATCCGTTGTATTAGTAACAT
- AlaProthrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAla GCCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCTCTTATAGC CGGGGTGTGACACCCCTCCTACTATGACTACTGGGTAAAGAAATGGCAGGAATATCGC

4806 PFLM1, 4807 DRA3,

ArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGlu

3589 DRA3, 3600 SAC2,

3611 ALWN1, 3655 PFLM1,

LeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThrPheAsp TIGGTGIATTCCACCACCTCACGCAGTGCTTGCCAAAGGCAGAAGAAAGTCACATTTGAC AACCACATAAGTGGTGGAGTGCGTCACCAACGGTTTCCGTCTCTTTCAGTTAAACTG

3681 DRA3.

- ArgleuGInValleuAspSerHistyrGlnAspValleuLysGluValLysAlaAlaAla
  3722 AGACTGCAAGTTCTGGACAGCCCTTTACCAGGACGTTAAAGGAGGTTAAAGCAGCGGCG
  TCTGACGTTCAAGACCTGTGGGTAATGGTCCTGCATGAGTTCCTCCAATTTCGTGGCGC
- SerLysvalLysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrProProHis
  3782 TCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCAGCCCCCACAC
  AGTTTTCACTTCCGATTGAAGGATAGGCATCTCCTTCGAACGTCGGACTGCGGGGGTGTG

3816 HIND3,

SerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArgLysAla
3842 TCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACCTCCGTTGCCATGCCAGAAAGGC
AGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTACGGTCTTTCCGG

3875 AAT2, 3890 BGLI,

- ValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrProfleAsp
  3902 GTAACCCACATCAACTCCGTGTGGAAGACCCTTCTGGAAGACAATGTAACACCAATAGC
  CATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGTTATCTG
- ThrThrILeMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGlyArgLys
  3962 ACTACCATCATGGCTAAGAACGAGGTTTTCTGCTCTCAGCCTGAGAAAGGGGGGGTCGTAAG
  TGATGGTAGTACCGATTCTTGCTCCAAAAGACGCAGTTCGGCACTCTTCCCCCCAGCATTC
- ProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMetAlaLeu CCAGCTCGTCTCATCGTGTTCCCCGATCTGGGCGTGGCGGAAAGATGGCTTTG GGTCGAGCAGAGTAGCACAAGGGGCTAGACCCGCACGGCACAGCGTTTTCTACCGAAAC
- TyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPheGlnTyr
  4082 TACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCCTCCTACGGATTCCAATGATATG
  ATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCCTTCGAGGATGCCTAAGGTTATG
- SerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThrProMet 1142 TCACCAGGACAGGGGTTGAATTCCTGCAAGCGTGGAAGTCCAAGAAAACCCCAATG AGTGGTCCTGTCGCCCAACTTAAGGAGCACGTTGCGACCTTCAGGTTCTTTTGGGTTAC

4160 ECORT.

GlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIleArgThr 4202 GGGTTCTCGTATACCCGCTGCTTTGACTCCACAGTCACTAGAGCGACATCCGTACG CCCAAGAGCATACTATGGGGACGAAACTGAGGTGTCAGTGACTCTCCGTGTAGGCATG ThrAlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGln
2942 ACGGTAACCATGACTCCCCTGATGGTGAGGCTAAAGGCCAACCTCCTATGGAGGCAG
TGGGGATTGGTACTGAGGGGACTACGACTCGATTATCTCCGGTTGGAGGATACCTCCTC

2966 ESP1, 2969 SACI,

GluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSer
3002 GAGATGGGCGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGACTCC
CTCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTTTGTTTCACCACTAAGACCTGAGG

PheAspProLeuValAlaGluGluAspGluArgGluTleSerValProAlaGluIleLeu TTCGATCCGCTTGTGGCGGAGGAGGACGAGCGGGAGATCTCCGTACCGCAGAAATCCTG AAGCTAGGGGAACACCGCCTCCTCTGCTCGCCCTCTAGAGGCATGGGCGTCTTTAGGAC

3096 BGL2,

ArglysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnPro
3122 CGGAAGTCTCGGAGATTCGCCCAGGCCCCTGCCCGTTTGGGCGCGGCGCGGACTATAACCCC
GCCTTCAGAGCCTCTAAGCGGGTCGGGAACGGGCAAACCCGCCGGCCTGATATTGGGG

3143 ALWN1, 3164 EAG1 XMA3,

ProLeuValGluthrTrpLysLysProAspTyrGluProProValValHisGlyCysPro CCGCTAGTGGAGACGTGGAAAAGCCCGACTACGAACCACCTGTGGTCCATGGCTGCCCG GCCGATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGACACCAGGTACCGACGGGC

3217 HGIE2, 3229 NCOI,

LeuProProProLysSerProProValProProProArgLysLysArgThrValValLeu
3242 CTTCCACCTCCAAGTCCCCTCCTGTGCCTCCGCCTCGGAAGAGCGGACGGTGGTCCTC
GAAGGTGGAGGTTTCAGGGGAGGACACGGAGGCGAGCCTTCTTCGCCTGCCACCAGGAG

ThroluserThrLeuserThrAlaLeuAlaGluLeuAlaThrArgSerPheGlySerSer
3302 ACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAGCTTTGCAGCTCC
TGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGTGGTCTTCGAAACCGTCGAG

3332 SACI, 3346 HIND3.

CysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGlyGluPro
3422 TGCCCCCCGACTCCGACGCGAGCCTATTCCTCCATGCCCCCCCTGAGGGGACCT
ACGGGGGGGCTAGGCTTCCGACTCAGGATAAGGAGCTACGGGGGGGACCTCCCCTCGGA

3437 EAM11051,

GlyAspFroAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsnAlaGlu
3482 GGGGATCCTGAGCAGCGGGTCATGGTCAACGGTCAGTAGTGAGGCCAACGCGGAG
CCCCTAGGCCTAGAATCGCTGCCCAGTTGCCAGTTGCCAGTCATCACTCCGGTTGCGCTC

3484 BAMHI, 3485 BSAB1, 3487 BSPE1,

ASPValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrProCysAla 3542 GATGTCGTGTCAATGTCTTACTTTGGACAGGCCCACTCGTCACCCGTGCGCC CTACAGCACAGGACGAGTACAGAATGAGAACCTGTCGGCGTGAGCAGTGAGGCAG 3589 DRA3, 3600 SAC2,

3611 ALWN1, 3655 PFLM1.

LeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThrPheAsp
TTGGTGTATTCCACCACCTCACGCAGTGCTTGCCAAAGGCAGAAGAACTACACATTGAC
AACCACATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGTCTTCTTCAGTGTAAACTG

3681 DRA3.

- ArgLeuGlnValLeuAspSerHistyrGlnAspValLeuLysGluValLysAlaAlaAla
  3722 AGACTGCAAGTTCTGGACAGCCATTACCAGGACGTTCCAGAGGGTTAAAGCAGCGGCG
  TCTGACGTTCAAGACCTGTCGGTAATGGTCCTGCATGAGTTCCTCCATTTCGTCGCCG
  TCTGACGTTCAAGACCTGTCGGTAATGGTCCTGCATGAGTTCCTCCAATTTCGTCGCCGC
- SerlysvallysalassleuleuservaldludlualacysserleuthrProProHis
  TCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCAGCCCCCACAC
  AGTTTCACTTCCGATTGAAGGATAGGCATCTCCTTCGAACGTCGGACTGCGGGGTGTG

3816 HIND3,

SERALALYSSELLYSPHEGLYTY/GLYALALYSASPVALATGCYSHLSALATGLYSALA
3842 TCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGGCCCCGTTGCCATGCCAGGAAAGGCC
AGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTTACGGTCTTTCGGG

3875 AAT2, 3890 BGLI.

- ValThrHisileAsnSerValTrpLysAspLeuLeuGluAspAsnValThrProfleAsp
  3902 GTAACCCACATCAACTCCGTGTGGAAGACCCTTCTGGAAGACAATGTAACACCAATAGAC
  CATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGTTATCTG
- ThrThrILeMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGlyArgLys
  3962 ACTACCATCATGCTAAGAACGAGACTTTTCTSCCTTCAGCCTAGAAGGGGGGTGCTAAG
  TGATGGTAGTACCGATTCTGCTCCAAAAGACGCAAGTCGGACTCTTCCCCCCAGGATTC
- ProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMetAlaLeu 4022 CCAGCTCGTCCTCGTCTCCCGATCTGGGCCTGGGCGTGTGGGAAAGATGGCTTTG GGTCGAGCAGGTAGCACAAGGGGCTAGACCCGCACGGGCACAGCGTTTTCTACCGAAAG
- TyrAspValValThrLysLeuProLeuAlaValMetolySerSerTyrGlyPheGlnTyr
  TACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCTCCTAGGATTCCAATAC
  ATGCTGCACCAATGTTTCGAGGGAACCGGCACTACCCTTCGAGGATGCCTAAGGTTATG
- SerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThrProMet
  1142 TCACCAGGACAGCGGTTGAATTCCTCCTGCAAGCGTGGAAGTCCAAGAAAACCCCAATG
  AGTGGTCCTGTCGCCCAACTTAAGGAGCACGTTCGCACCTTCAGGTTCTTTTGGGGTTAC

4160 ECORT.

GlyPheSerTyxAspThrArgCysPheAspSerThrValThrCluSerAspIleArgThr 4202 GGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGGGACATCCTACG CCCAAGAGCATACTATGGGCAGGAAACTGAGGTTCAGTGACTCTCGCTGTAGGCATGC

- LysGlyValTrpArgGlyAspGlyIleMetHisThrArgCysHisCysGlyAlaGluIle
  2342 AAGGGGTCTGGCGAGGGGACGGCATCATGCACACTCGCTGCCACTGTGAGCTGAACT
  TCCCCCAGACCGCTCCCCTCCGTAGTACTGTGAGCGACGGTGACACTCCACTCTAG
- ThrGlyHisValLysAsnGlyThrMetArgIleValGlyFroArgThrCysArgAsnMet
  ACTGGACATGTCAAAAACGGGACGATGAGGAACGTGCTGGGACCTGCAGGAACATG
  TGACCTGTACAGTTTTTGCCCTGCTACTCCTAGCAGGATCCTGGAGGTCTCTTGAC
  - 2425 BSAB1, 2441 AVR2, 2448 SSE83871, 2449 PSTI,
- TFDSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeuProAla
  TGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCTGTAACCCCCTTCCTGCG
  ACCTCACCCTGGAAGGGGTAATTACGGATGTGTGCCCGGGGAATGGGGGAAGGACGC
  - 2480 ASE1, 2497 APAI.
- ProAsnTyThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGln 2522 CCGAACTACACGTCGGCCTATGGAGGGTGTCTGCAGAGGAATACGCTAGGAGATAAGGCAG GGCTTGATGTGCAAGGGGATACCTCCCAAGAGGTCTCCTTATGCACCTCTATTCCGG
  - 2553 PSTI.
- ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLyscysProcysGln
  2582 GTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTTAAATGCCCGTGCCAG
  CACCCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTTACGGGCACGGGA
  - 2594 DRA3.
- ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaPro GTCCCATCGCCCGAATTTTTCACGAGATTGGACGGGGTGCGCCTACATAGGTTTGGCCC CAGGGTAGCGGGCTTAAAAGTGTCTTAACTGCCCCACGCGGATGTATCCAAACCGGGG
- ProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrPro 2702 CCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGAGTAGGACTCCAGGATACCCG GGGACGTTCGGGAACGACCCTCCTCCATAGTAAGTCTCATCCTGAGGTGCTTATGGGC
  - 2757 HGIE2.
- ValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeu
  GTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACTGGCCGTGTTGACGTCCATGCTC
  CATCCCAGCGTTAATGGAACGTCGGGCTTGGCCTGCACCGGACAATGCAGGTACCAG
  CATCCCAGCGTTAATGGAACGTCGGGCTTGGCCTGCACCGGACAATGTGAGGTACCAG
  - 2809 AAT2.
- - 2850 EAG1 XMA3,
- ProSerValAlaSerSerSerAlaSerGlnLeuSerAlaFroSerLeuLysAlaThrCys
  2882 CCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGC
  GGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAAGGTAGAGAGTTCCGTTGAACG
  - 2889 BALI, 2903 NHEI,

1794 ESP1,

GlyAlaAlaTleGlySerValGlyLeuGlyLysValLeuTleAspIleLeuAlaGlyTyr
GGGGCGCCATCGGCAGTGTTGGACTGGGAGGTCTCCATAGACATCCTTGCAGGGTAT
CCGCGGGGTAGCCGTACACCCGTTCCAGGAGTATCTGTAGGAACCTCCCATA

1802 KAS1 NARI.

GlyAlaGlyValAlaGlyAlaLeuValAlaPheLysTleMetSerGlyGluValProSer GGGGGGGGGGGGGGGGGGCTCTTGTGGCATTCAAGATCATGAGGGTGAGGTCCCCTCC CGGGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAGGGGAG

1878 SACI, 1899 BSPH1.

ThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValValGly
1922 ACGAAGGACCTGGTCAATCTACTGCCCGCCCTCCTCGCCCGAGCCCTCGTAGTCGGC
TGCCTCCTGGACCACTTAGATGACGGGGGTAGGAGAGCGGCCTCGGGAGATCAGCCG

1928 TTH3I.

ValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaValGlhTrp GTGGTCTGTGCAGCAATACTGCGCCGGGAGGTGGCCGGGCGAGGGGGGAGGTGCAGTGG CACCAGACACGTCGTTATGAGCGGGCCTGCACCGGGCCCGTCCCCCTCACGTCACC

2004 NAEI, 2017 SMAI XMAI,

MetAsnArgleuileAlaPheAlaSerArgGlyAsnHisValSerProThrHisTyvval
2042 ATGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCCCACGACTACTGTG
TACTTGGCCGACTATCGGAAGCGGACCCCTTGGTACAAAGGGGGTGCGTGATCAC

2067 SMAI XMAI, 2093 DRA3,

ProGluserAspAlaAlaAlaArgValThrAlaTleLeuserSerLeuThrValThrGln
2102 CCGGAGGCGATGCAGCTGCCCGCGTCACTGCCATACTCAGCGAGCCTCACTGTAACCCAG
GGCCTCTCGCTACGTCGACGGGGCGAGTGACGGTATGAGTCGTCGGAGTGACATTGGGTC

2115 PVU2, 2159 ALWN1,

LeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSerGlySer 2162 CTCCTGAGGCGACTGCACCAGTGGATAGCTCGGAGTGTACCACTCCGTTCC GAGGACTCCGCTGACGTGGTCACCTATTCGAGCCTCACATGGTGAGGTAGGAGGCCAAGG

2164 MST2, 2220 ECON1,

- TTPLEUARGASPITETPASPTTPITECYSGIUVALLEUSERASPPHELYSTHTTPLEU
  TGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGGCGACTTGGCTA
  ACCGATTCCCTGTAGACCCTTATAGGCTCCACAACTCGCTGAAATTCTGGACCAT

2285 ESP1, 2300 PVU2, 2310 BAMHI,

ThralaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGln
ACCGCTAACCATGACTCCCCTGATGCTGAGCTCATGAGGCCAACCTCCTATGGAGGCAG
TGGCGATTGGTACTCAGGGGACTACCACTCGAGTATCTCCGGTTGGAGGATACCTCCGTC
2966 ESP1, 2969 SACI,

GluMetGlyGlyAsnIleThrArgValGluserGluAsnLysValValIleLeuAspSer GAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAACAAAGTGGTGATTCTGGACTCC CTCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTTTGTTTACACCATAAGACCTGAGG

PheAspProLeuValAlaGluGluAspGluArgGluTleSerValProAlaGluTleLeu TTCGATCCGCTTGTGGCGGAGGAGGAGGAGGAGGAGATCTCCGTACCGCGAGAATCCTG AAGCTAGGCGAACACCGCTCCTCCTGCTCGCCTCTTAGAGCATGGGCGTCTTTAGGAC

3096 BGL2,

3143 ALWN1, 3164 EAG1 XMA3,

ProLeuValGluthrTrpLysLysProAspTyrGluProProValValHisGlyCysPro CCGCTAGTGGAGACGTGGAAAAAGCCCGACTACGAACCACCTGTGGTCCATGGCTGCCCG GGCGATCACCTCTGCACCTTTTCCGGCTGATGCTTGGTGGACACCAGGTACCGACGGC

3217 HGIE2, 3229 NCOI,

ThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGlySerSer
ACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGCAGCTC
TGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGTGTCTTCGAAACCGTCGAG

3332 SACI, 3346 HIND3.

CysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGlyGluPro TGCCCCCCGACTCCGACGCCTGAGGCCTATTCCTCCATGCCCCCCCTGAGGGGAGCCT ACGGGGGGGCTAAGGATCAGGATAAGGAGTACGGGGGGACCTCCCCTCGGA

3437 EAM11051,

GlyAspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsnAlaGlu
GGGGATCCGGATCTTAGCGACGGGTCATGGTCAACGGTCAGTAGTGAGGCCAACGCGGAG
CCCCTAGGCCTAGGATCGCTGCCCAGTACCAGTTGCCAGTCATCACTCCGGTTGCGCCTC

3484 BAMHI, 3485 BSAB1, 3487 BSPE1,

AspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrProCysAla 3542 GATGTGGTGGTGAATGTCTTACTCTTGGACAGGGGCACTGGTGACCCGGTGGGC CTACAGCACAGACGAGTTACAGAATGAGAAGCGTGTGCGGGTGAGCAGGGGGACGCGG

- LysGlyValTrpArgGlyAspGlyIleMetHisThrArgCysHisCysGlyAlaGluIle
  2342 AAGGGGGTCTGGCGAGGGGACGGCATCATGCACACTGGCTGCCACTGTGGAGCTGAGATC
  TTCCCCCGAGCCGCTCCCCTGCGTAGTACGTGTGAGCCTGAGTGACACTCAGACTTAG
- ThrGlyHisValLysAsnGlyThrMetArgIleValGlyProArgThrCysArgAsnMet
  ACTGGACATGTCAAAAACGGACGATGAGGATCGTCGGTCCTAGGACCTCCAGGAACATGT
  TGACCTGTACAGTTTTTGCCCTGCTACTCCTAGCAGCCAGGATCCTGGACGTCCTTGTACTG
  - 2425 BSAB1, 2441 AVR2, 2448 SSE83871, 2449 PSTI,
- TTPSerGlyThrPheProlleAsnAlaTyrThrThrGlyProCysThrProLeuProAla
  TGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCCTGTACCCCCCCTTCCTGCG
  ACCTCACCTGGAAGGGGTAATTACGGATGTGGTGCCCGGGGACATGGGGGGAAGGACGC
  - 2480 ASE1, 2497 APAI.
- ProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGln
  CCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAATACGTGAGAGTAAGGCAG
  GGCTTGATGTGCAAGGGCGCATACCTCCCACAGAGGTTCCTTATGCACCTCTATTCCGTC
  - 2553 PSTI,
- ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGln 2582 GTGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTTAAATGCCCGTGCCAG CACCCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTTACGGGCACGGTC
  - 2594 DRA3.
- ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaPro GTCCCATCGCCCGAATTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGCGCCC CAGGGTAGCGGGCTTAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAACGCGGG
- ProcysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrPro CCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAAGAGTAGGACTCCACGAATACCCG GGACGTTCGGGAACGACCCTCCTCCATAGTAAGTCTCATCCTGAGGTGCTTATGGGC
  - 2757 HGIE2.
- ValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeu
  2762 GTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTTGACGTCCATGCTC
  CATCCCAGCGTTAATGGAACGTCGGGCTTGACCTGCACCAGCTACAGAGTACCAG
  - 2809 AAT2.
- - 2850 EAG1 XMA3.
- ProSerValAlaSerSerSerAlaSerGinLeuSerAlaFroSerLeuLysAlaThrCys
  2882 CCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTAAGGCAACTTGC
  GGGAGACACCGGTCGAGGAGCGATCGGTCGATAGGCGAGGATAGAGATTCCGTTGAAGG

2889 BALI, 2903 NHEI,

1794 ESP1,

GlyAlahlafleGlySerValGlyLeuGlyLysValLeufleAspileLeuAlaGlyTyr GGGCCGCCATCGGCAGTGTTGGACTGGGGAAGGTCCTCATAGACATCCTTGCAGGTAT CCGCGGGGGTAGCCCTTCCAGGACTATCTGTAGGAACTCCCATA

1802 KAS1 NARI.

GlyAlaGlyValAlaGlyAlaLeuValAlaPreLys1leMetSerGlyGluValProSer GGCGCGGGGGGGGGGGGCTCTTGTGGCATTCAAGATCATGAGGGTGAGGTCCCTCC CCGCGCCCGCACCAGAACACCGTAAGTCTATGATCTCCCACTCCAGGGGAG CCGGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTATGATCTCGCACT

1878 SACI, 1899 BSPH1,

ThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValValGly
ACGAAGGACCTGGTCAATCTACTGCCGCATCCTTCGCCCGAGCCCTTCGTAGTCGGC
TGCCTCGTGACCACTTAGATGACGGGGGTAGGACAGCGGCCTCGGGGACTACGCGG
TGCCTCCTGGACCACTTAGATGACGGGGGTAGGACAGCGGCCT

1928 TTH3I,

ValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaValGlnTrp GTGGTCTGTGCAGCAATACTGCGCCGGGCAGCGTGGCCCGGGCGAGGGGCAGTGCAGTGG CACCAGACACGTCGTTATGACGCGGCCCTGCACCGGGCCCGCTCCCCCGTCACGTCACC

2004 NAEI, 2017 SMAI XMAI.

MetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisvalSerProThrHisTyrVal 2042 ATGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCCCACGCACTACCTG TACTTGGCCGACTATCGGAAGCGGACCCCTTGGTACAAAGGGGGTGCGTGATCGA.

2067 SMAI XMAI, 2093 DRA3,

ProGluserAspAlaAlaAlaArgValThrAlaIleLeuserSerLeuThrValThrGln
CCGGAGGAGGCGGCCGCCGCGCACACTGCCATACTCAGCAGCCTCACTGTAACCCAG
GGCCTCTCGCTACGTCGACGGGCGCAGTGACGGTATGAGTCCTCGGAGTGAATTGGGTC

2115 PVU2, 2159 ALWN1,

LeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSerGlySer 2162 CTCCTGAGGCGACTGCACCAGTGGATAAGCTCGGAGTGTACCACTCCATGCTCCAGGTTCC GAGGACTCCGCTGACGTGGTCACCTATTCGAGCCTCACATGGTGAGGTACGAGGCCAAGG

2164 MST2, 2220 ECON1,

2285 ESP1, 2300 PVU2, 2310 BAMHI,

# FIG. 21-Page 4

ProThrLeuRisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluILe CCCACCTCCATGGGCCAACACCCCTGCTATACAGACTGGGGGGTGTTCAGAATGAAATG GGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCCCGACAAGTCTTACTTTAG

1150 NCOI.

ThrLeuThrHisProValThrLysTyrIleMetThrCysMetSerAlaAspLeuGluVal
1202 ACCCTGACGCACCCAGTCACCAAATACATCATGCATGCCTGTCGGCCGACCTGGAGGTC
TGGGACTGCGTGGGTCAGTGGTTTATGTAGTACTCTAGGTACAGCGGGTGGACCTCCAG

1230 BSPH1, 1234 DRD1, 1237 AVA3, 1245 EAG1 XMA3, 1250 DRD1,

- ValThrSerThtTpValLeuValGlyGlyValLeuAlahlaLeuAlahlaTyrCysLeu GTCACGAGCACCTGGTGCTCGTTGGCGGCGTCTGGTTGGCCGCGGTATTGCCTG CAGTGCTCGTGGACCCACGAGCAACCGACGCAGCAAACCGGCGCATAACGGAC

1369 NAEI.

ProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGlnHisLeu CCTGACAGGGAAGTCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACTTA GGACTGTCCCTTCAGGAGATGGCTCTCAAGGTACTCTCCCTTCTCACGAGAGTCGTGAAT

1385 DRD1.

- ProfyrileGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGlyLeu
  1442 CCGTACATCAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGGCAG
  GGCATGTAGCTCGTCACTACTACGAGGGGCTCGTCAAGGTTCGTCTCGGGAGCCGGAG
- LeuGlnThrAlaSerArgGlnAlaGluValIleAlaFroAlaValGlnThrAsnTrpGln
  1502 CTGCAGACCGCCCCGTCAGCCAAGGGTTATCGCCCCTGCTGTCACAACTGCCAA
  GACGTCTGGCGCAGGCAGTCCGTCTCCAATAGCGGGACAACAGGTCTGGTTGACCGTT

1502 PSTI, 1507 TTH3I,

LysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheTleSerGlyIleGlnTyrLeu
1562 AAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAATACTTG
TTCAGCTCTGGAAGACCCGCTTCGTATACACCTTGAATAGTAGCACCATATGTTATGAAC

1565 XHOI, 1586 NDEI.

AlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPhethrAla
1622 GCGGCTTGTCAACGCTGCTGGTAACCCCGCCATTGGTGACTTGATGGCTTTACAGGC
CGCCGAACAGTTGCGACGACCATTGGGGGGTAACGAAGATACTACGAAAATTGC

1643 BSTE2, 1677 ALWN1 PVU2,

AlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGlyGlyTrp GCTGTCACCAGCCCACTAACCACTAACCCTCCTCTACACATATTGGGGGGTGG CGACAGTGGTCGGGTGATTGGTGATGGGTGGGAGGAGAAGTTGTATAAGCCCCCCAC GCACAGTGGTCGGGTGATTGGTGATGGGTGGAGGAGAAGTTGTATAA

- SerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsnAlaVal
  182 TCAAAGAAGTGCGACCGAACTCGCCCCAAAGCTGGTCGCATTGGGATCAATGCCGTG
  AGTTTCTTTCTTCAGCTGGTGGTTGAGCAG
- AlaTyrTyrArgGlyLeuAspValSerValTleProThrSerGlyAspValValValVal 542 GCCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCAGCGGCGATGTTGTCGTCGTG CGGATGATGGCGCCAGAACTGCACAGGCAGTAGGGCTGGTCGCCGCTACAACAGCAGCAC

550 SAC2, 560 DRD1.

AlathraspalaLeuMetThrGlyTyrThrGlyAspPheAspSerVallleAspCysAsn
602 GCAACCGATGCCCTCATGACCGGCTATACCGCGCACTTCGACTCGGTGATAGACTCCAAT
CGTTGGCTACGGGAGTACTGGCCGTATATGGCGCTGAAGCTGAGCCACTATTGGACGTA

615 BSPH1.

- ThrCysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGluThrIle
  662 ACGTGTGTCACCCAACAACAGTGGATTCAGCCTTCACCCTTCACCATTGAGACAATC
  TGCACACAGTGGGTTCTCAGCTAAAGTCGGAACTGGGATGGGAAGTGGTAACTCTGTTAG
- ThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLys
  ACCTTCCCCAGATGCTGTCTCCGCACTCAACGTTCGGGCAGGACTGCCAGGGGAAG
  TGCGAGGGGTTTACGACAGAGGGGTGAACTTCAACGCCCTCTAACGTCCCCCTTAC
- ProGJyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAspSerSer 782 CCAGGCATCTACAGATTTGTGGCACCGGGGGAGGCCCCTCCGGCATGTTCGACTCGTCC GGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGAGGCCGTACAAGCTGAGCAG

816 BGLI, 833 DRD1.

ValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAlaGluThr 842 GTCCTCTGTGAGTGCTATGACGCAGGCTGTGCTTGGTATGAGCTCAGCGCGCCGCAGAGCT CAGGAGACACTCACGATACTGGGTCCGACAGGAACCATACTGGAGTGCGGGGGCTCTGA

881 SACI,

ThrValArgLeuArgAlafyrMetAsnfhrProGlyLeuProValCysGlnAspHisLeu 902 ACAGTTAGGCTACGAGCGTACATGAACACCCCGGGCTTCCCGTGTGCAGGCTCTCTTGTGATCCAATCCGATGCTGTTAGTAGTCAATCCGATGCTGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCCTGGTAGAA

931 SMAI XMAI,

GluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGln 62 GAATTTTGGGAGGCGTCTTTACAGGCCTCACTCATATAGATGCCACTTTCTATCCAG CTTAAAACCCTCCCGCAGAATGTCCGGAGTGAGTATATCTACGGGTGAAAGATAGGGTC

985 STUI.

ThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCysAla
1022 ACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAGCCACCGTGTGCGCT
TGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGCATGGTTCGGTGGCACACGCGA

1069 DRA3,

ArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeuLys
AGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATTCGCCTCAAG

TOCOGRATTOO	CCCACCCCCTACCI	COCOMCCMCTACAC	********************************	-

- ProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluIle
  CCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAATGAAATC
  GGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTACTTTAG
  - 1150 NCOI,
- - 1230 BSPH1, 1234 DRD1, 1237 AVA3, 1245 EAG1 XMA3, 1250 DRD1,
- ValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeu GTACAGGACCTGGGTGCTGTGTGGGGGCTCCTGGCTGCTTGTGCCGCGTATTGCCTG CAGTGCTCGTGGACCCACGAGCAACCGCCGCAGACGGAACCGGACGATACCGGCG
- SerThrGlyCysValVallleValGlyArgValValLeuSerGlyLysProAlaIleIle
  1322 TCAACAGGCTGCGTGATACATGGGCAGGGTCGTCTTGTCCGGGAAGCCGGCAATCATA
  AGTTGTCCGAGGCACCAGTATCACCCGTCCCAGCAGAACAGGCCCTTCGGCCGTTAGTA
  - 1369 NAEI,
- - 1385 DRD1,
- LeuGlnThrAlaSerArgGlnAlaGluValTleAlaFroAlaValGlnThrAsnTrpGln
  1502 CTGCAGACCGCGTCCCGTCAGGCAAGGGTTATCGCCCTGCTGTCTCCAACTGGCAA
  GACGTCTGGCGCAGGCAGTCCCTCCCAATAGCGGGACGACAGGTCTGGTTGACCGTT
  - 1502 PSTI, 1507 TTH3I.
- LysLeuGluthrPheTrpAlaLysHisMetTrpAsnPheTleSerGlyIleGlnTyrLeu
  AAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAATACTTG
  TTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCACCCTATGTTATGAAGC
  - 1565 XHOI, 1586 NDEI.
- AlagiyleuSerThrleuProglyAsnProAlaIleAlaSerleuMetAlaPheThrAla 1622 GCGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGCTTTTACAGCT CCCCCGAACAGTTGCGACGACCATTGGGGCGGTAACGAAGTAACTACCGAAAATGTGGA
  - 1643 BSTE2, 1677 ALWN1 PVU2,
- AlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGlyGlyTrp GCTGTCACCAGCCCATAACCACTAGCCAAACCCTCCTCTTCAACATATTGGGGGGGTGG CGACAGTGGTGGGTGATTGGTAGTGGGTGGAGAAGTTGTAAACCCCCCCACC

TOTOLOGOTOD AGA	CCTGTCGGTAATGGTC	つかくぐみ ずぐみ ぐずかくぐり	こっしゃ かかかかつこうかっこう

SerlysVallysAlaAsnleuLeuSerValGluGluAlaCysSerLeuThrProProHis
782 TCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGGAACGCTGACGCCCCCACAC
AGTTTTCACTTCCGATTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGGGTGTG

3816 HIND3,

SerAlaLysSerLysPheGlyTyrGlyAlaLysAspWalArgCysHisAlaArgLysAla TCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGAAAGGCC AGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCTTTCCGG

3875 AAT2, 3890 BGLT.

- ValThrHisileAsnSerValTrpLysAspLeuLeuGluAspAsnValThrProIleAsp
  GTAACCCACATCAACTCCGTGTGGAAGAGACCTTCTGGAAGACAATGTAACACCAATAGAC
  CATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGTTATTTT
- ThrThrILeMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGlyArgLys
  3962 ACTACCATCATGCTAAGAACGAGGGTTTTTTCTCCTTCAGCCTTAAGAAGGGGGTCTCATAG
  TGATGGTAGTACCGATTCTTGCTCCAAAAGACGAGTTGGACTCTTCCCCCAGCATTC
- ProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMetAlaLeu CCAGCTCGTCTCATCGTGTTCCCCGATCTGGGCGTGCGCGTGTGGCGAAAAGATGGCTTTG GGTGGACCAGAGTAGCACAAGGGGCTAGACCCGCACACGCTTTTCTACCGAAAC
- TyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPheGlnTyr
  4082 TACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCTCCTACGGATTCCAATAC
  ATGCTGCACCAATGTTTTCGAGGGGAACCGCACTACCCTTCGAGGATGCCTAAGGTTATG
- SerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThrProMet
  1142 TCACCAGGACAGCGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACCCCAATG
  AGTGGTCCTGTGCGCCAACTTAAGGAGCACGTTCGCACCTTCAGGTTCTTTTTGGGGTTAC

4160 ECORI.

GlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIleArgThr 4202 GGGTTCTCGTATACCCGCTGCTTTGACTCCACAGTCACTAGAGAGCGACATCCGTACG CCCAAGAGCATACTATGGGCGACGAAACTGAGGTTCAGTGACTCTCCGTGTAGGCATGC

4229 DRD1, 4236 ALWN1,

GluGluAlaIleTyrcIncyscysAspLeuAspProGlnAlaArgValAlaIleTysSer 4262 GAGGAGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCGGGCCATCAAGTCC CTCCTCGGTTAGATGGTTACAACACTGGAGCTGGGGGTTCGGGGGCACCGGTAGTTCAGG

4301 BGLI, 4308 BALI,

LeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGly
4322 CTCACCGAGAGGCTTTATGTTGGGGCCCTCTTACCAATTCAAGGGGGGGAGAATTGCGGC
GAGTGGCTCTCCGAAATACAACCCCCGGGAGAATAGTTAAGTTCCCCCCTCTTGACGCCG

4345 APAI.

TyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCys
4382 TATCGCAGGTGCCGCGGAGGGGCGTACTGACATAGCTGTGGTAACACCCTCACTTGC
ATAGGTCCAGGGGGGCTGGCGGCATGACTGTTGATGGACACCATTGTGGAGTGGAGTAG

# FIG. 18-Page 7

- SerLysLysLysCysAspGluLéuAlahlaLysLeuValAlaLeuGlyIleAsnAlaVal 182 TCAAAGAAGAAGTGCGACGAACTCGCCGCAAAGCTGGGTGGCATTGGGCATCAGTGCCGTG AGTTTCTTCTTCAGGGTGCTTGAGGGGGGTTTGGACCAGCGTAACCGTAACCGTAACTGTAACGGCAC
- AlatyrtyrargólyLeuhapValSerValTleProThrSerGlyAspValValValVal 542 GCCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCAGCGGCGATGTTGTCGTCGTG CGGATGATGGGCCAGAACTGCACAGGCAGTAGGGCTGGTCGCCGCTACAACAGCAGCAC

550 SAC2, 560 DRD1.

AlathraspalaLeuMetThrGlyTyrThrGlyAspPheAspSerValIleAspCysAsn
602 GCAACCGATGCCCTCATGACCGGCTATACCGCGCACTTCGACTGGTGATAGACTGCAAT
CCTTGGCTACGGGAGTACTGGCCGATATGGCGCTGAAGCTAGACCACTATTGACGTTA

615 BSPH1,

- ThrCysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGluThrIle
  662 ACGTGTGTCACCCTAGCCTTAGCCTTAGCCTTACCATTCAGACATTCA
  TGCACACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGAATGGAAGTGAACTGTAACTCTCTTAC
- ThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLys
  AGGCTCCCCAAGATGCTGTCTCCGCACATCAACGTCGGGCAGGACTGGCAGGGGAAG
  TGCGAGGGGTTTACGACAAGGGGGTGAGTTGCAGCCCCCTTAC
- ProGJyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAspSerSer 782 CCAGGCATCTACAGATTTGTGGCACCGGGGGAGGCCCCTCCGGGATGTTCGACTGGTC GGTCCGTAGATGTCTAAACACGGTGGCCCCCTGGGGGAGGCCGTACAAGCTGAGCAG

816 BGLI, 833 DRD1,

881 SACI.

ThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAspHisLeu
902 ACAGTTAGGCTACCAGGGTACATGAACACCCGGGGGCTTCCGTGTGCAGGACCATCTT
TGTCAATCCGATGGTCGCATGTACATGAGCCCCGAAGGGCCACAGGGTCCTTGTGTAGAA

931 SMAI XMAI,

GluPheTrpGluGlyWalPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGln 642 GAATTTTGGGAGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATCCCAG CTTAAAACCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAGATAGGGTG

985 STUI.

ThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCysAla
1022 ACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTGGGT
TGTTTCGTCTCACCCCTCTTGGAAGGAATGGACTGCATGGTTGGGTGGTTGGGTGGACAGCGGA

1069 DRA3.

ArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeuLys
1082 AGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAACTGTTTGATTCGCCTCAAG

MetAlaAlaTyrAlaAlaGlnGlyTyrLysValLeuValLeuAsr
AGCTTACAAAACAAAATGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACTCAAG
TCGAATGTTTTGTTTTACCGACGTATACGTCGAGTCCCGATATTCCACGATCATGAGTTC

- 1 HIND3, 24 NDEI, 52 SCAI,
- ProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyILeAsp 62 CCCTCTGTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGATCGAT GGGAGAACGACGTTGTGACCCGAAACCACGATGTACAGGTTCCGAGTACCCTAGCTA
  - 116 CLAI,
- ProAsnIleArgThrGlyWalArgThrIleThrThrGlySerProIleThrTyrSerThr
  122 CCTAACATCAGGACCGGGTGAGAACAATTACCACTGGAGCCCCATCACGTACTCACC
  GGATTGTAGTCCTGGCCCCACTTGTTAATGGTGACCGGGGTAGTGCATGAGGTGG
- TYTGIYLYSPHeLEUALAASpGIYGIYCYSSETGIYGIYALATYTASpILEILEILECYS
  182 TACGGCAAGTTCCTTGCCGACGGCGGGTGTCGGGGGGCGCTTATGACATAATAATTTGT
  ATGCCGTTCAAGGAACGGCTGCCGCCACGAGCCCCCCGAATACTGTATTATTAAACA
- AspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuAspGln 242 GACGACTGCCACTCCACGGATGCCACATCCATCTTTGGGCATTGGCATGTCCTTGACCAA CTGCTCACGGTGAGGTGCCTACGGTGTAGGTGAACCCGTAACCGTGACAGAACTGGTT
- AlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrProProGlySerVal
  302 GCAGAGACTGCGGGGGCGAGCTGGTTGTGCTCGCCACCGCCACCCCTCCGGGCTCCGTC
  CCTCTCTGACGCCCCCGCTCTGACCAACACGAGCGGTGGGGAGGCCCGAGGCAG
  - 303 ALWN1,
- ThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGlyGluIleProPhe
  362 ACTSTGCCCCATCCCAACATCGAGGAGTTGCTCTTCCACCACCGGAGAGTCCCTTTT
  TGACACGGGTAGGGTTGTAGGCTAACT

5449 APAI,

GlyWalArgAlaThrArgLysThrSerGluArgSerGlnProArgGlyArgArgGlnPro
GGTGTGGGGGGGAGAAGAATGACTTCCGAGGGGGGCAACCTCGAGGTAGACGTCAGCCT
CCACACGCGCGTGCTCTTTCTGAAGGCTCGCAGCGTTGGAGCTCAATCTGCAGTCGGA

5467 BSSH2, 5478 XMNI, 5502 XHOI, 5511 AAT2,

1leProLysAlaArgArgProGluGlyArgThrTrpAlaGlAProGlyTyrProTrpPro
ATCCCCAAGGCTCGTCGGCCCGAGGGCAGGACCTGGGCCTCAGCCCGGTCCTTGGCC
TAGGGGTTCCGAGCAGCAGCAGCACCGGTCCTTGGACCGGGCCCATTGGGAACCGGG

5548 ALWN1, 5558 ESP1, 5564 SMAI XMAI, 5568 KPNI,

- LeuTyrGlyAsnGluGlyCysGlyTrpAlaGlyTrpLeuLeuSerProArgGlySerArg
  CTCTATGGCAATGAGGCTGCGGGTGGGCGGGATGGCTCTGTCTCCCCTGGGCTTCTGG
  GAGATACCGTTACTCCGAGGCCCACCGGCCTACCGAGGACAGAGGGGCACCGAGAGC
- ProSerTrpGlyProThrAspProArgArgArgArgAsnLeuGlyLysValIleAsp CCTAgCTGGGGCCCACAGACCCCCGGCGTAGGTCGGCATTTGGGTAAGGTCATCGAT GGATCGACCCGGGGTTGTTGGGGGCCCCATCCAGCGCGTTAAACCCATTCAGTAGCTA

5650 APAI, 5696 CLAI,

ThrLeuThrCysGlyPheAlaAspLeuMetGlyTyrIleProLeuValOC AM
5702 ACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCTATATAGTCGAC
TGGGAATGCAGCCGAAGCGGCTGGAGTACCCCATGTATGGCGAGCAGATTATCAGCTG

5724 HGIE2, 5755 SALI,

FIG. 21-Page 10

- 3122 CGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCCGTTTGGGCGCGGCCGGACTATAACCCC
  GCCTTCAGAGCCTCTAAGCGGGTCCGGGACAGCCCGGCCTGATATTGGGG
  3143 ALWN1, 3164 EAGI XMA3,
- ProLeuValGluThrTrpLysLysProAspTyrGluProProValValHisGlyCysPro
  3182 CGGCTACTGGAGACTGGGAAAAGCCCGACTACGAACCACCTGTGGTCCATGGCTGCCCG
  GGCGATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGACACCAGGTACCGACGACG
  GGCGATCACCTCTGCACCTTTTTTCGGGCTGATGCTTGGTGACACCAGGTACCGACGGGC
  - 3217 HGIE2, 3229 NCOI,
- ThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGlySerSer
  ACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGCAGCTCC
  TGACTTAGTTGGGATAGATGAACGGAACCGGCTCGAGCGGTGTCTTCGAAACCGTCGAG
  - 3332 SACI, 3346 HIND3,
- CysProProAspSerAspAlaGluserTyrSerSerMetProProLeuGluGlyGluPro
  3422 TGCCCCCCGACTCCGACGCTGAGTCCTATTCCTCCATGCCCCCCCTGGAGGGGAGCCT
  ACGGGGGGGTGAGGCTGAGGTAGGATTAAGGAGGTACGGGGGGACCTCCCCCTCGGA
  - 3437 EAM11051,
- GlyAspProAspLeuserAspGlySerTnpSerTnrValSerSerGluAlaAsnAlaGlu
  3482 GGGATCCGGATCTTAGCGACGGGTCATGGTCAACGGTAGTAGTGAGGCCAACGCGGAG
  CCCCTAGGCCTAGGATCGCCAGTACCAGTTGCCAGTCATCACTCCGGTTGCCCTC
  - 3484 BAMHI, 3485 BSAB1, 3487 BSPE1,
- AspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrProCysAla 3542 GATGTCGTGTGCTCAATGTCTTACTCTTGGACAGGGGCACTCGTCACCCGGTGCGC CTACAGCACACGACAGTTACAGAATGAGAACCTGTCCGGTGAGCAGTGGGGCACGCGG
  - 3589 DRA3, 3600 SAC2,
- AlaGluGluGlnLysLeuProIleAsnAlaLeuSerAsnSerLeuLeuArgHisHisAsn
  3602 GGGGAAGAACGAAACTGCCATCAATGCACTAAGCAACTGGTTGCTACGCACACAAT
  CGCCTTCTTGTCTTTGACGGGTAGTTACGTGATTCGTTGAGCAACGATGCAGTGGTGTTA
  - 3611 ALWN1, 3655 PFLM1,
- LeuValTyrserThrThrSerArgSerAlacysclnArgGlnLysLysValThrPheAsp
  TTGGTGTATTCCACCACCTCACGCAGTGCTTGCCAAAGGCAGAAGAAAGTCACATTTGAC
  AACCACATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGTCTTCTTTCAGTGTAAACTG
  - 3681 DRA3.
- ArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAlaAlaAla
  3722 AGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGGAGGTTAAAGCAGCGGCG

ProAsnTyrTh:PheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGln
2522 CCGAACTACACGTTCGCGCTATGGAGGGTGTCTCCACAGGAATACGTGGAGATAAGGCAG
GGCTTGATGTGCAAGCGCGATACCTCCCACAGACGTCTCCTTATGCACCTCTATTCCGTC
2553 PSTI,

ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGln 2582 GTGGGGGACTTCCACTACGTGACGGGTATGACTACTACAATCTTAAATGCCCGTGCCAG CACCCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTTACGGGCACGGTC

2594 DRA3.

ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaPro GTCCCATCGCCCGAATTTTTCACAGAATTGGACGGGTGGGCTGACATAGGTTTGGGCCC CAGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAACGCCGG

ProCyslysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrPro CCCTGCAAGCCCTTCCTCCGGGAGGAGGTATCATTCAGACTAGGACTCCACGAATACCCG GGGACGTTCGGGAACGACCCTCCTCCTAGTAAGTCTCATCCTGAGGTCTTATGGC TOTAGT

2757 HGIE2.

2809 AAT2,

2850 EAG1 XMA3,

ProSerValAlaSerSerSerAlaSerGinLeuSerAlaFroSerLeuLysAlaThrCys
CCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGC
GGGAGACACCGGTCGAGGAGCCGATGGGTGAGGAGTAGAGACTTCCGTTGAAGG

2889 BALI, 2903 NHEI,

ThrAlaAshHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGln
ACCGCTAACCATGACTCCCCTGATGCTGATGAGGCAGCCCCTCCTATGGAGGCAG
TGGCGATTGGTACTGAGGGACTACGACTGAGTATCTCCGGTTGGAGGATACCTCCGT

2966 ESP1, 2969 SACI.

GluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSer GAGATGGGGGGCAACATCACCAGGGTTGAGTCAGAAAACAAGTGGTGATTCTGGACTCC CTCTACCCGCCGTTGTAGTGGTCCCAACTAGTCTTTTGTTTACACCATAAGACCTGAGG

PheAspProLeuValAlaGluGluAspGluArgGluTleSerValProAlaGluTleLeu
TTCGATCCGCTTGTGGCGAGGAGGAGGAGGAGATCTCCGTACCCGCAGAAATCCTG
AAGCTAGGCGAACACCGCCTCCTCTGCTCGCCCTCTAGAGGCATGGGCGTCTTTAGGAC

3096 BGL2.

ArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnPro

MetAlani	aTurblabl	aGlaGlyTy	rt veValter	Walloune

- - 1 HIND3, 24 NDEI, 52 SCAI,
- ProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyIleAsp 62 CCCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGATCAGT GGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCCTAGCTA
  - 116 CLAI,
- ProAsnileArgThrGlyValArgThrIleThrThrGlySerProIleThrTyrSerThr
  122 CCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTACTCCACC
  GGATTGTAGTCCTGGCCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGCATGAGGTG
- TyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleIleCys
  182 TACGCCAAGTTCCTTGCCGACGGCGGGTGCTCGGGGGGCGCTTATGACATAATAATTTGT
  ATGCCGTTCAAGGAACGGCTGCCGCCCACGAGCCCCCCGCGATACTGTATTATTAAACA
- ASPGJUCYSHISSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuAspGln 242 GACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATTGGCATGTCCTTGACCAA CTGCTCACGGTGAGGTGCCTACGGTGTAGGTAGAACCCGTAACAGCGTGACAGGAACTGGT
- AlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrProProGlySerVal 302 GCAGAGACTGCGGGGGCGAACTGGTTGTGCTCGCCACCGCCACCCCTCCGGGCTCCGTC CCTCTCTGACGCCCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGGAGGCCGAGGCAG
  - 303 ALWN1.
- ThrValProHisProAsnileGluGluValAlaLeuserThrThrGlyGluIleProPhe
  362 ACTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCCTTTT
  TGACACGGGGTAGGGTTGTAGCTCCTCCAACGAGACAGGTGGTGGCCTCTTAGGGAAAA

4862 AGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACTCCATAGAA TCCCTGGTCGAACTTGTCCGGGAGCTAACGCTCTAGATGCCCCGGACGATGAGGTATCTT

4893 BGL2.

ProLeuAspleuProProlleIleGlnArgLeuHisGlyLeuSerAlaPheSerLeuHis 4922 CCACTGGATCTACCTCCAATCATTCAAGACATCCATGGCCTCAGCGATTTCACATCCAC GGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGGATTCGCGTAAAAGTGAGGTG

4954 NCOI.

SerTyrSerProGlyGluIleAsnArgvalAlaAlaCysLeuArgLysLeuGlyValPro
4982 AGTTACTCTCCAGGTGAAATCAATAGGGTGGCCGCATGCCTCAGAAAACTTGGGGTACCG
TCAATGAGAGGTCCACTTTAGTTATCCCACCGGCGTAGGGAGTCTTTTGAACCCCATGGC

5015 SPHI, 5035 KPNI,

ProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGly
5042 CCCTTGGGAGCTTGGAACACCGGGCCCGGACCCTCCGCCTAGGCTTCGGCTAGAGGA
GGGAACGCTGAACCTCTGTGGCCCGGGCCTGCAGGGCGCATCCGAAGACCGGTCTCCT
GGGAACGCTGAACCTCTGTGGCCCGGGCCTGCAGG

5064 APAI, 5091 BALI.

GJyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLys 5102 GGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGCAGTAAGAACAAAGCTCAAG CCGTCCCGACGGTATACACGGTTCATGGAGAAGTTGACCCGTCATTCTTGTTTCCAGTTA

5113 NDEI,

5174 NOTI, 5175 EAG1 XMA3, 5182 BALI, 5186 PVU2,

5240 DRA3.

LeuLeuLeuLeuAlaAlaGlyValGlyTleTyrLeuLeuProAsnArgMetSerThrAsn
CTACTCCTGCTTGCTGCAGGGGTAGGCATCTACCTCCTCCCAACCGAATGAGCACGAAT
GATGAGGACGAACGACCTCCCCATCCGTAGATGGAGAGGGGTTGGCTTACTCGTGCTTA

5295 PSTI.

ProlysProGlnArglysThrLysArgAsnThrAsnArgArgProGlnAspVallysPhe
CCTAAACCTCAAAGAAGACAACGTAACACCAACCGGCCGCCGCAGGACGTCAAGTTCAAG
GGATTTGGAGTTTCTTTCTGGTTTGGATTGTGTGCCGCCGGCGTCCTGCAGTTCAAG

5380 NOTI, 5381 EAG1 XMA3, 5390 AAT2, 5401 SMAI XMAI.

ProGlyGlyGlyGlnIleValGlyGlyValTyrLeuLeuProArgArgGlyProArgLeu CCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGGCCTTAGATTG GGCCCACCGCCAGTCTAGCAACCACCTCAAATGAACAACGGGGCTCCCCGGGATCTAAC 4229 DRD1, 4236 ALWN1,

GluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIleLysSer 4262 GAGGAGCAATCTACCAATGTTGTGACCTCGACCCCCAGCCCGTGGCCATCAAGTCC CTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCGGGGCACCGGTAGTTCAGG

4301 BGLI, 4308 BALI,

LeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGly
4322 CTCACCGAGAGGCTTTATGTTGGGGCCCTCTTACCAATTCAAGGGGGGGAGAATACGCGC
GAGTGGCTCTCCGAAATACAACCCCCGGGAGAATAGTTAAGTTCCCCCCTCTTGACGCCG

4345 APAI,

- TYPATGATGCYSATGALASETGLYVAILeuThrThrSerCysGlyAsnThrLeuThrCys
  4382 TATCGCAGGTGCCGCGGGGGGGGGTACTGACAACTAGCTGTGGTAACACCCTCACTTGC
  ATAGGGTCACGGGGGGCTGGCCGCATGACTGTTGATGGACACCATTGTTGGAGTGAACG
- Tyr11eLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlAAspCysThrMetLeuVal TACATCAAGGCCCGGCAGCCTGTCGAGCCGCAGGGCTCCAGGACTGCCACCATGCTCGTG ATGTAGTTCCGGGCCCGTCGGACAGCTCGGGGTCCCGAGGTCCTGACGTGGTACGAGCAC

4452 SMAI XMAI,

CysGlyAspAspLeuValValIleCysGluSerAlaGlyValGlnGluAspAlaAlaSer 4502 TGTGGCGACGACTTAGTCGTTATCTGTGAAAGCCGGGGGGTCCAGGAGGACGGGCGAGG ACACCGCTGCTGAATCAGCAATAGACACTTTCGGGCCCCCAGGTCCTCCTGCGCCGCTG

4508 DRD1, 4511 TTH31,

- LeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspProProGln
  4562 CTGAGAGCCTTCACGGATACTGACCAGGTACTCCGCCCCCCCGGGGACCCCCAGA
  GACTCTCGGAAGTGCCTCGGATACTGGTCCATGAGGCGGGGGGACCCCTGGGGGGTATT
- ProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAlaHisAsp CCAGAATACGACTTGGACTCATAACATCATCCTCCTCCACGTGTCAGTCGCCCACGAC GGTCTTATGCTGAACCTCGAGTATTCTAGTACGAGGAGGTTGCACAGTCAGCGGGTGCTA

4637 SACI,

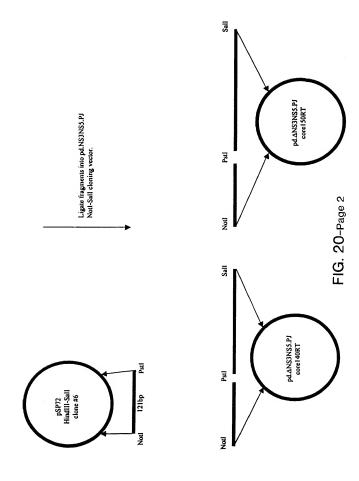
GlyAlaGlyLysArgValTyrTyrLeuThrArgAspFroThrThrProLeuAlaArgAla 4682 GGGGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCCCTACAACCCCCCTCGGAGAGCT CCGGGACCTTTCTCCCAGATGATGGAGTGGGATGTGGGGGGAGCCCTCTCGA

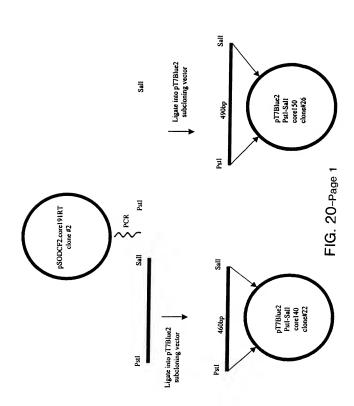
4731 NRUI,

- AlatrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMetPhe
  GCGTGGGAGACAGCAAGACACACTCCAGTCAATTCCTGGCTAGGCAACATAATCATGTTT
  GCGACCCTCTGTGTGTGTGAGGTCAGTTAAGGACCGATCGTTGTATTATGACATA
- AlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAla 4802 GCCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCCTTATAGCC CGGGGTGTGACACCCGCTCCTACTATGACTACTGGTAAAGAAATCGCAGGAATATCGG

4806 PFLM1, 4807 DRA3,

 $\label{lem:argAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGluIl$ 





ThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValValGly
ACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTAGTCGGC
TGCCTCCTGGACCAGTTAGATGACGGGCGGTAGGAGAGCGGGCCTCGGGAGCATCAGCCG

1928 TTH3I.

2004 NAEI, 2017 SMAI XMAI.

MetAsnArgLeuIleAlaPheAlaSerArgGIyAsnHisValSerProThrHisTyrVal
ATGAACCGGCTGATAGCCTTCGCCTCCGGGGGACCATGTTTCCCCACGCACTACGTG
TACTTGGCCACTATCGGAAGCGGCCCCTTGGTACAAAGGGGGTGGTGATGCAC

2067 SMAI XMAI, 2093 DRA3,

ProGluserAspAlaAlaAlaArgValThrAlaTleLeuserSerLeuThrValThrGln
CCGGAGAGCGATGCAGCTGCCGCGCGTCACTGCCATACTCAGCAGCCTCACTGTAACCCAG
GGCCTCTCGCTACGTCGACGGGGGAGTGACGGTATGAGTCTCTGGAGTGACATTGGGTC

2115 PVU2, 2159 ALWN1,

LeuLeuArgArgleuHisGlnTrpILeSerSerGluCysThrThrProCysSerGlySer CTCCTGAGGCGACTGCACCAGTGGATAAGCTCGGAGTGTACCACTCCATGCTCCAGGTTCC GAGGACTCCGCTGACGTGGTACCTATTCGAGCCTCAGGTTGAGGTACAGGCCAAGG

2164 MST2, 2220 ECON1,

- TFDLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThrTrpLeu
  TGGCTAAGGGACATCTGGGACTGGATATGCGAGCTGTGAGCGACTTTAAGACCTGGCTA
  ACCGATTCCCTGTAGACCCTTAACGCTCCACAACTGGCTGAAATTCTTGGACCCAT
- LysAlaLysLeuMetProGlnLeuProGlyILeProPheValSerCysGlnArgGlyTyr
  AAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCTTTTGTGTCTGCAGCGCGGTAT
  TTTGGATTCGACTGACGGACCCTAGGGGAACACAGGACGGTGCGCCCATA

2285 ESP1, 2300 PVU2, 2310 BAMHI,

- LysGlyValTrpArgGlyAspGlyIleMetHisThrArgCysHisCysGlyAlaGluIle
  AAGGGGTCTGGCGAGGGGACGGCATCATGCACACTGCGCCCACTGTGGAGCTGAGATC
  TTCCCCCAGACGGTCCCCTGCGGTAGTACTGTGAGCGAGGGTGACACCTGACTCTGA
- ThrGlyHisValLysAsnGlyThrMetArgIleValGlyProArgThrCysArgAsnMet 2402 ACTGGACATGTCAAAACGGGACGGTGGAGGATCGTGGTCTTAGGACCTGCAGGACATG TGACCTGTACAGTTTTGCCCTGCTACTCCTAGCAGGACAGGATCCTGGAGGTCCTTGTAC

2425 BSAB1, 2441 AVR2, 2448 SSE83871, 2449 PSTI,

TTPSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeuProAla
TGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGCCCCTGAACCACCGGAATGGGGGAAGGACG
ACCTCACCCTGGAAGGGGTAATTACGATGTGGTGCCCGGGGAATGGGGGAAGGACGC

2480 ASE1, 2497 APAI,

SerThrGlyCysValValIleValGlyArgValValleuSerGlyLysProAlaIleIle
1322 TCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTGTCCGGAAACCGGCAATACTA
AGTTGTCCGACGCACCAGTATCACCGGTCCCAGCAGAACAGGCCCTTGGGCGTTAGTAT

1369 NAEI.

ProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGlnHisLeu CCTGACAGGAAGTCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCGACTTA GGACTGTCCCTTCAGGAGATGGCTCTCAAGGTACTCTACCTTCTCACGAGAGTGTGAAT

1385 DRD1,

- LeuGlnThrAlaSerArgGlnAlaGluValTleAlaFroAlaValGlnThrAsnTrpGln
  1502 CTGCAGACCGCGTCCCGTCAGGCAAGAGGTTATCGCCCCTGCTGTCACAACTGGCAA
  GACGTCTGGCGCAGGCAGTCCTCCAATAGCGGGACGACAGGTCTGGTTAACCGTT

1502 PSTI, 1507 TTH3I,

LysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheTleSerGlyIleGlnTyrLeu
AAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAATACTTG
TTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCACCCTATGTTATGAAGC

1565 XHOI, 1586 NDEI,

AlaGlyLeuSerThrLeuProGlyAsnProAlaTleAlaSerLeuMetAlaPheThrAla
GCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTACAGCT
GCCCGAACAGTTGCGACGACCATTGGGGCGGTAACGAAGTAACTACCAAAATGTCA

1643 BSTE2, 1677 ALWN1 PVU2,

- AlaValThrSerProLeuThrThrSerGinThrLeuLeuPheAsnIleLeuGlyGlyTrp GCTGTCACCAGCCACTAACCACTAGCCAAACCCTCCTCTCTAACATATTGGGGGGTGG CGACAGTGGTCGGGTGATTGGTGATCGGTTTTGGGAGGAGAAGTTGTATAACCCCCCACC
- ValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGlyLeuAla
  1742 GTGGCTGCCCAGCTCGCCGCCCCGGTGCCCTTCTGCGGCGTGGCCTTAGCT
  CACCGACGGATCGACCGACCGATCACGAATCAC

1794 ESP1,

GlyAlaAlaIleGlySerValGlyLeuGlyLysValleuIleAspIleLeuAlaGlyTyr GGGCCCCCATCGCAGTGTTGGAGCTGGGGAAGTCTCATAGACATCCTTGCAGGTAT CCGCGGGGTAGCCCTCACAACCTGACCCCTTCCAGGAGTATCTTATGGAACCTCCCATA

1802 KAS1 NARI,

GlyAlaGlyValAlaGlyAlaLeuValAlaPeLysTleMetSerGlyGluValProSer GGGGGGGGGGGGGGGGGCTCTTGTGGCATTCAAGATCATGAGGGTGAGGTCCCCTCC CGGGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAGGGGAGG

1878 SACI, 1899 BSPH1,

- LysGlyValTrpArgGlyAspGlyIleMetHisThrArgCysHisCysGlyAlaGluIle
  2342 AAGGGGTCTGGCGAGGGACGCCATCATGCACACTGCTGCCACTGTGGAGCTGAGATC
  TTCCCCCAGACGGTCCCCTGCCGTAGTACGTGTGAGCGTAGGTGTACCTGACTTAG
- ThrGlyHisValLysAsnGlyThrMetArgIleValGlyProArgThrCysArgAsnMet
  ACTGGACATGTCAAAACGGGACGATGAGGATCGTGGTCATGAGACTGCAGGAACATG
  TGACCTGTACAGTTTTTGCCCTGCTACTCCTAGCAGCAGGATCCTGGAGCTCTTGTAC
  - 2425 BSAB1, 2441 AVR2, 2448 SSE83871, 2449 PSTI,
- TFPSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeuProAla
  TGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCCTGTACCCCCTTCCTGCG
  ACCTCACCCTGGAAGGGGTAATTACGGATGTGTGCCCGGGGAATGGGGGAAGGACGCA
  - 2480 ASE1, 2497 APAI,
- ProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGIn 2522 CCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAATAAGGTGGAGATAAGGCAG GCTTGATGTGCAAGCGGATACCTCCCACAGAGGTCTCCTTATGCACCTCTATTCCCCT
  - 2553 PSTI.
- ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGln 2582 GTGGGGGACTTCCACTAGCTGCAGGGTATGACTACTAACAATCTCAAAATGCCCGGTGCAG CACCCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTTACGGGCACGGTC
  - 2594 DRA3.
- ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaPro GTCCCATCGCCCGAATTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGGGCCC CAGGGTAGCGGGGTTAAAAGTGTCTTAACTGCCCCACGGGGATGTATCCAAACGCGGG CAGGGTAGCGGGTTAAAAGTGTCTTAACTGCCCCACGGGATGTATCCAAACGCGGG
- ProcyslysProLeuleuArgGluGluValSerPheArgValGlyLeuHisGluTyrPro CCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGGATAGGACTAGGACTCCACGAATACCG GGGACGTTCGGGAACGACCCCTCCTCCATAGTAAGTCCTATCCTGAGGTGCTTATGGGC
  - 2757 HGTE2.
- Val61ySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeu
  GTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACTGGCCGTTTGACGTCCATGCTC
  CATCCCAGCGTTAATGGAACGCTCGGGCTTGACCTGCACCGGCACAACTGCAGGTACGAG
  CATCCCAGCGTTAATGGAACGCTCGGGCTTGACCTGCAC
  - 2809 AAT2,
- - 2850 EAG1 XMA3.
- PROSETVAIALSERSERALASSERGINLEUSERALABROSERLEULYSALATHRCYS
  CCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGC
  GGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGAGAAGAGTTCCGTTGAAGG
  - 2889 BALI, 2903 NHEI,

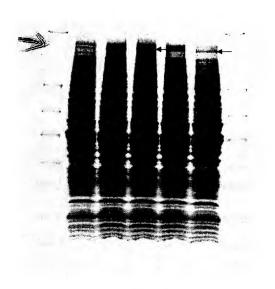


FIG. 19

ValAlahlaGinLeuAlaAlaProGlyAlahlaThralaPheValGlyAlaGlyLeuAla
1742 GTGGCTGCCCAGCTGCCCCCCGGTGCCGCTACTGCCTTTGTGGGCGCTGCTTAGCT
CACCGACGGTGCAGCGGATGACGGAAACACCCGCGACGAATGA

1794 ESP1,

GlyAlaAlaTleGlySerValGlyLeuGlyLysValLeuTleAspIleLeuAlaGlyTyr
GGGCGCCATCGGCAGTGTTGGACTGGGAGGTCTCATAGACATCCTTGCAGGGTAT
CCGCGGCGGTAGCCGTTCCAGGAGTATCTGTAGGAACCTCCCATA

1802 KAS1 NART.

1878 SACI, 1899 BSPH1,

ThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValValGly
ACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTAGTCGGC
TGCCTCCTGGACCACTTAGATGACGGCGGTTAGGAGAGCGGCCTCGGGAGCATCAGCCG

1928 TTH3I.

ValValCyshlahlaIleLeuArgArgHisValGlyProGlyGluGlyAlaValGlnTrp GTGGTCTGTGCAGCAATACTGCGCCGGGCGAGGTGCAGGGGGCAGTGCAGTGG CACCAGACACGTGTTATGACGCGGCCTGCAACCGGGCCCGCTCCCCCCTTACGTCACC

2004 NAEI, 2017 SMAI XMAI,

2067 SMAI XMAI, 2093 DRA3,

ProGluSerAspAlaAlaAlaArgValThrAlaTleLeuSerSerLeuThrValThrGln 2102 CCGGAGAGCGAGCCGCCCCGCTCACTGCCATACTCAGCAGCCTCACTGTAACCCAG GGCCTCTCGCTACGTCGACGGGGCAGTGACGGTATGAGTCGTCGGAGTGACATTGGGTC

2115 PVU2, 2159 ALWN1,

LeuleuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSerGlySer CTCCTGAGGCGACTGCACCAGTGGATAAGCTCGGAGTGTACCACTCCATGCTCCGGTTCC GAGGACTCGCCTGACGTGGTCACCTATTCGAGCCTCACATGGTGAGGTACAGGCCAAGG

2164 MST2, 2220 ECON1.

TPDLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThrTrpLeu
TGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTGAGCGACTTTAAGACCTGGCTA
ACCGATTCCCTGTAGACCCTTAACGTCCACATCTCGGTCGATAT

2285 ESP1, 2300 PVU2, 2310 BAMHI.

## FIG. 17-Page 4

PROTHILEUHISGLYPROTHPFOLEULEUTYPARGLEUGLYAL&VALGINASHGLUILE CCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGGTGTTCAGAATGAAATG GGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCCGGACAAGTCTTACTTTAG

1150 NCOI.

1230 BSPH1, 1234 DRD1, 1237 AVA3, 1245 EAG1 XMA3, 1250 DRD1,

- ValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeu
  GTCACGAGCACCTGGGTGCTCGTTGGCCGCTTGGTTGGCTCGTTTGCCCG
  CAGTGCTGGTGGACCCACGAGCAACCGCCGCAGGAACCGGCGCATAACGGAC
  CAGTGCTGGTGGACCCACGAGCAACCGCCGCAGGAACCGGCGCATAACGGAC
- SerThrGlyCysValValILevalGlyArgValValLeuSerGlyLysProAlaIleILe
  1322 TCAACAGGCTGCGTGATACATGGGCAGGGTCGTCTTGTCCGGGAAGCCGGCAATCATC
  AGTTGTCCGAGGCACCAGTATCACCCGTCCCAGCAGAACAGGCCCTTCGGCCGTTAGTAT

1369 NAEI.

ProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGlnHisLeu CCTGACAGGGAAGTCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGGACTTA GGACTGTCCCTTCAGGAGATGGCTCTCAAGGTACTCTCCCTTCTCACGAGAGTCGTGAAT

1385 DRD1,

- ProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGlyLeu
  1442 CCGTACATCGAGCAAGGGTGATGGTCGCCGAGCAGTACAAGCAGAGGCCCTCGGCAGC
  GGGATGTAGCTGGTTCCCTACTACGAGGGGCTCGTCAAGTTCGTCTTCGTGGAGACCGGAG
- LeuGlnThrAlaSerArgGlnAlaGluValTleAlaFroAlaValGlnThrAsnTrpGln
  1502 CTGCAGACCGCCCCGCTAGGCAAGAGGTTATCGCCCCTGCTGTCACAACTGGCAA
  GACGTCTGGCGCAGGCAATCCGTCTCCAATAGCGGGACGACAGGTCTGGTTGACCGTT

1502 PSTI, 1507 TTH3I,

LysleugluthrPhetrpAlaLysHisMetTrpAsnPheIleSerglyIlegIntyrLeu
AAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAATACTTG
TTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCACCCTATGTTATGAAG

1565 XHOI, 1586 NDEI.

AlagiyleuSerThrleuProGlyAsnProAlaIleAlaSerLeuMetAlaPheThrAla
1622 GCGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTCCATTGATGCCTTTTACAGCT
CGCCCGAACAGTTGCGACGACCATTGGGGCGGTAACGAAGTAACTACGAAAAATGTGA

1643 BSTE2, 1677 ALWN1 PVU2,

- ThrCysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGluThrIle
  662 ACGTGTGTCACCCAGACAGTCGATTTCAGCCTTGACCCTTCACCATTGAGACAATC
  TGCACACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGGATGGAAGTGGTAACTCTGTTAG
- ThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLys
  722 ACGCTCCCCAAGATGCTGTCTCCCGCACTCAACGTGGGCAGGACTGCCAGGGGAAG
  TGCGAGGGGGTTTACGACAGAGGGCGTGAGTTGCAGCCCGTCCTGACCGTCCCCTTC
- ProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAspSerSer
  782 CCAGGCATCTACAGATTTGTGGCACCGGGGGAGGCCCCTCCGGCATGTTCGACTCGTC
  GGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGGGGAGGCCGTACAAGCTGAGCAGG
  - 816 BGLI, 833 DRD1,
- ValleuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAlaGluThr 842 GTCCTCTGTGAGTGCTATGAGCGAGGGTGTGCTTGGTATGAGGCTACGCCCCCCGAGAC CAGGAGACACTCACGATACTGGGTCGCACGAACCATACTCGAGTGCGGGGGGTCTCTA
  - 881 SACI.
- ThrValArgLeuArgAlaTyzMetAsnThrProGlyLeuProValCysGlnAspHisLeu
  902 ACAGTTAGGCTACGAGGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCATCTT
  TGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACAGGTCCTGGTAGAA
  - 931 SMAI XMAI.
- GluphetrpGluGlyValphethrGlyLeuthrHisIleAspAlaHisPheLeuSerGln
  962 GAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCACTTTCTATCCAG
  CTTAAAACCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAGATAGGGTC
  - 985 STUI,
- - 1069 DRA3.
- ArgAlaGinAlaProProProSerTrpAspGinMetTrpLysCysLeuIleArgLeuLys
  1082 AGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATTCGCCCCAAGT
  TCCGGAGTTGGGGAGGGGGTAGCACCTTGGTCTACAAACTAAGCGAAGTC
- ProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluILe 1142 CCCACCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAATGAAATC GGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTACTTTAG
  - 1150 NCOI,
- - 1230 BSPH1, 1234 DRD1, 1237 AVA3, 1245 EAG1 XMA3, 1250 DRD1,
- ValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeu
  1262 GTCACGAGCACCTGGTTGCCGTTGGCGGCTCCTTGGCTGCTTTGCCGCGTATTGCCTG

5642	ProSerTrpGlyProThrAspProArgArgArgSerArgAsnLeuGlyLysValIleAspCCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTCATCGATGGATCGACCCCGGGGTGTCTGGGGGCCGCATCCAGCGCGTTAAACCCATTCCAGTAGCTA
	5650 APAI, 5696 CLAI,
5702	$\label{thm:cysGlyPheAlaAspLeuMetGlyTyrIleProLeuValGlyAlaProLeu} ACCCTTACGTGCGGCTCCGACCCTCATGGGGTACATACCGCTCCTCGGCGCCCCCTCTT TGGGAATGCACGCCGAAGCGGCTGGAGTACCCCATGTATGGCGAGCAGCCCGGGGGAGAA$
	5724 HGIE2, 5750 KAS1 NARI, 5756 ECON1,
5762	GlyGlyAlaAlaArgAlaLeuAlaHisGlyValArgValLeuGluAspGlyValAsnTyr GGAGGCGCTGCCAGGGCCCTGGCGCATGCCGTCCTGGAACACGGCGTGAACTAT CCTCCGCGACGGTCCCGGGACCGCACCCCAGGCCCAAGACCTTTGATA
	5772 BSTXI, 5775 APAI,
5822	AlaThrGlyAsnLeuProGlyCysSerOC AM GCAACAGGGAACCTTCCTGGTTGCTCTTAATAGTCGAC

CGTTGTCCCTTGGAAGGACCAACGAGAATTATCAGCTG

5854 SALI,

FIG. 18-Page 10

ProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGly
CCCTTGCGAGCTTGGAGACACCGGGCCCGGAGCGTCCGCGTAGGCTTCTGGCCAGAGGA
GGGAACGCTCGAACCTCTGTGGCCCGGGCCTCGCAGGCGCGGATCCGAAGACCGGTCTCCT
5064 APAI, 5091 BALI,
GlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLys
GGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAAGCTCAAA
CCGTCCCGACGGTATACACCGTTCATGGAGAAGTTGACCCGTCATTCTTGTTTCGAGTTT
5113 NDEI,

5174 NOTI, 5175 EAG1 XMA3, 5182 BALI, 5186 PVU2.

5240 DRA3.

LeuleuleuleuAlaAlaGlyValGlyIleTyrLeuleuProAsnArgMetSerThrAsn
CTACTCCTGCTTGCTGCAGGGGTAGGCATCTACCTCCCCAACCGAATGAGCACGAAT
GATGAGGACGAACGACGTCCCCATCGGTAGATGAGGAGGGGTTGGGTTTGCTGTGCTGT

5295 PSTI,

ProLysFroGlnArgLysThrLysArgAsnThrAsnArgArgProGlnAspValLysPhe 5342 CCTAAACCTCAAAGAAGACCAAACGTAACACCAACCGGGGCCCGAGGAGCTCAAGGTTC GGATTTGGAGTTTCTTGTTGGTTTGCATTGTGGTTGGCCGCGGGGTCCTGCAGTTCAAG

5380 NOTI, 5381 EAG1 XMA3, 5390 AAT2, 5401 SMAI XMAI,

ProGlyGlyGlyGlnIleValGlyGlyValTyrLeuLeuProArgArgGlyProArgLeu CCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGGCCCTAGATTG GGCCCACCGCCAGTCTAGCAACCACCTCAAATGAACAACGAGGGGGTCCCCGGGATCTAGC

5449 APAI,

GlyValArgAlathrArgLysthrSerGluArgSerGlnProArgGlyArgArgGlnPro GGTGTGGGGGGGAGAGAAGACTTCCGAGGGGGGGAACCTCGAGGTAGAGGTCAGCCT CCACACGCGCGTGCTCTTTCTGAAGGCTCGCCAGCGTTGAGCTCCATCTGCAGTCGGA

5467 BSSH2, 5478 XMNI, 5502 XHOI, 5511 AAT2,

11eProLysalaArgArgProGluGlyArgThrTrpAlaGlnProGlyTyrProTrpPro ATCCCCAAGGCTCGTCGGCCCGAGGGCAGGACCTGGGCCTAGCCCGGGTACCCTTGGCCC TAGGGTTCCGAGCAGCGGCCCCCGTCCTTGGACCCGGCCCCATGGAACCGG

5548 ALWN1, 5558 ESP1, 5564 SMAI XMAI, 5568 KPNI,

LeuTyrGlyAsnGluGlyCysGlyTrpAlaGlyTrpLeuLeuSerProArgGlySerArg
CTCTATGGCAATGAGGCTSCGGGTGGGGGGGGGTGCTCTCTCCCCCTGGCTTCGG
GAGATACCGTTACTCCCGAGCCCCACCCCCCTACCGAGAGGGACAGAGGGCACCGAGAGC

### FIG. 18-Page 9

#### MetAlaAlaTyrAlaAlaGlnGlyTyrLysValLeuValLeuAsn

- - 1 HIND3, 24 NDEI, 52 SCAI,
- ProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyIleAsp
  62 CCCTCTGTTGCTGCAACACTGGGCTTTGGTGCTACATGTCCAAGGCTCATGGATCGAT
  GGGAGACAACGACGTTGTGACCCGAAACCACGATGTACACGGTTCCCAGTACCCTAGCTA
  - 116 CLAI,
- ProAsnIleArgThrGlyValArgThrIleThrThrGlySerProIleThrTyrSerThr
  122 CCTAACATCAGACCGGGGTGAGAACAATTACCACTGGCAGCCCATCAGGTACTCCACC
  GGATTGTAGTCCTGGCCCCACTCTGTTAATGGTGACCGTGGGGTAGTGGTGA
- TyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleIleCys
  182 TACGCCAAGTTCCTTGCCGACGGCGGTGCTCGGGGGGGCGCTTATGACAAATAATTTGT
  ATGCCGTTCAAGGAACGGCTGCCGCCACGGGCCCCCGGGAATACTGTATTAATAAACA
- AspGluCysHisSerThrAspAlaThrSerTleLeuGlyIleGlyThrValLeuAspGln 242 GACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATTGGCATTGTGCTGACCAA CTGCTCACGGTGAGGTGCCTACGGTGTAGGTAGAACCCGTAACCGTGACAGGAACTGGTT
- AlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrProProGlySerVal
  GCAGAGACTGCGGGGGCGAGACTGGTTGTGCTCGCCACCCCTCCGGGCTCCGTC
  CGTCTCTGACGCCCCCCCTCTGACCAACACGAGCGGTGGGGTGGGGAGGCCCGAGGCAG
  - 303 ALWN1.
- ThrValProHisProAsnIleGluGluValAlaLeuserThrThrGlyGluIleProPhe
  362 ACTGTGCCCCATCCCAACATCGAGGAGGTGCTCTGTCCACCACCGAGGAGATCCCTTTT
  TGACACGGGGTAGGGTTGTAGCTCCTCCAACGAGACAGGTGGTGGCCTCTTAGGGAAAA
- TyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeuIlePheCysHis 422 TACGCCAAGGCTATCCCCTCGAAGTAATCAAGGGGGGGAGACATCTCATCTTCTGTCAT ATGCGTTCGGATAGGGGGAGCTTCATTAGTTCCCCCCCCTGTGAGGATAAGAGAGAAGA
- SerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsnAlaVal
  482 TCAAAGAGAAGTCCGACCGAACTCCCCCCAAAGCTGGTCGCATTGGGCATCAATGCCGTG
  AGTTTCTTCTTCAGCGTGCTTGAGCGGGGTTTCGACCACACGTAACCCGTAGTTACGCGAC
- AlatyrtyrArgGlyLeuAspValSerValTleProThrSerGlyAspValValValVal 542 GCCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCAGCGGCGATGTTGTCGTCGTG CGGATGATGGCGCCAGAACTGCACAGGCAGTAGGGCTGGTCGCCGCTACAACAGCAGCAC
  - 550 SAC2, 560 DRD1,
- AlathraspalaleuMetthrclyTyrThrclyAspPheaspSerVallleAspCysAsn
  602 GCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGATTCCAAT
  CCTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAAGCACTATCTGACGTTA
  - 615 BSPH1,

- SerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsnAlaVal
  TCAAAGAAGAGTGCGACGAACTGCGCGAAAGCTGGCGATTGGGCATCGATTGGGCATCGTG
  AGTTTCTTCTTCAGGCTGCTTGAGGGGGGTTTGGACCAGGGTAACCGGTAGTTACGGCA
- AlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAspValValValVal 542 GCCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCAGCGGCGATGTTGTCGTCGTG CGGATGATGGCGCCAGAACTGCACAGCAGCTAGGGCTGGTCGCCGCTACAACAGCAGCAC

550 SAC2, 560 DRD1.

AlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerVallleAspCysAsn
GCAACCGATGCCCTCATGACCGGCTATACGGCGCACTCGACTCGGTGATAGACTGCAT
CCTTGCTACGGCAGATACTGCCGATATGACTGACCACTTATCTGACGTTA

615 BSPH1.

- ThrcysValthrGlnthrValAspPheSerLeuAspProThrPheThrIleGluThrIle
  662 ACGTGTCACCCAGACAGTCGATTTCAGCCTTAGCCTTACCATTGAGACAATC
  TGCACACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGGATGGAAGTGGTAACTCTTTTAG
- ThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLys
  ACCCTCCCCAAGATGCTGTCTCCCGCGACTCAACGTGGGGGACTGGGAGGGGATGGGGGGAGT
  TGGAGGGGGTTACGAAGGGGGGGGAGTTGCAACCGTTCCTGCCTTC
- ProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAspSerSer 782 CCAGGCATCTACAGATTTGTGGCACCGGGGGAGGCCCCTCCGGCATGTTCGACTCGTCC GGTCCGTAGATGTCTAAACACCGTGGCCCCCTTGCGGGAGGCCGTACAAGCTGAGCAGG

816 BGLI, 833 DRD1,

ValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAlaGluThr 842 GTCCTCTGTGAGTGCTATGAGCCAGGCTGTGCTTGGTATGAGCTCACGCCCGCGAGACT CAGGAGACACTCACGATACTGCGTCCGACACGAACCATACTTGGAGTGCGGGGGGTCTTGA

881 SACI.

ThrValArgLeuArgAleTyrMetAsnThrProGlyLeuProValCysGlnAspHisLeu
902 ACAGTTAGGCTACGGGACATCAACCCCCGGGGCTTCCCGTGTGCCAGGACCATCTT
TGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCCTGGTAGGA

931 SMAI XMAI.

GluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGln 962 GAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATCCAG CTTAAAACCCTCCCGCAGAAATGTCCGGAGTGAGTAATCTACGGGTGAAAGATAGGGTC

985 STUI.

ThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCysAla
1022 ACAAAGCAGAGTGGGGAAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGCT
TGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATGGTTCGGTGGGAACGCAA

1069 DRA3,

ArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeuLys
1082 AGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATTCGCCTCAAG

2522 CCGAACTACACGTTCGCGCTATGGAGGGGTGTCTGCAGAGGAATACGTGGAGATAAGGCAG
GGCTTGATGTGCAAGCGCGATACCTCCCACAGACGTCTCCTTATGCACCTCTATTCCGTC
2553 PSTI,

ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGln
GTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTTAAATGCCCGTGCCAG
CACCCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTTTACGGGCACGGTC
2594 DRA3,

ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaPro GTCCCATGCCCGAATTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGGCCC CAGGGTAGCGGGCTTAAAAGTGTGTTAAACTGCCCCACGCGAGTGTATCCAAACGCGGG

ProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrPro 2702 CCCTGCAAGCCCTTCCTGCGGGAGGAGGTATCATTCAGGATAGGACTCCACGAATACCCG GGGACGTTCGGGAACGACCCCTCCTTCCATAGTAAGTCATCCTGAGGTGCTTATGGGC

2757 HGTE2.

ValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeu
2762 GTAGGGTGGATTACCTTGCGAGCCCGAACCGGACTGGCCGTGTTGACGTCCATGCTC
CATCCCAGCGTTAATGGAAGCGTCGGGCTTGGCCTGCACCGGCACAACTGCAGGTACGAG

2809 AAT2.

ThraspProSerHisIleThrAlaGluALaALaGlyArgArgLeuAlaArgGlySerPro
2822 ACTGATCCTCCCATATAACAGCAGAGGGCGGCGGGGAGGTTGGCGAGGGATCACCC
TGACTAGGGAGGGTATATTGCTCTCCGCGGCCCGCTTCCAACCGGTCCCCTAGTGGG

2850 EAG1 XMA3,

ProSerValhlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCys 2882 CCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGC GGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGTTGAACG

2889 BALI, 2903 NHEI,

ThralaasimisaspserproaspaladiuleulledlualaasileuleutrpargGlm 2942 ACCGCTAACCATGACTCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAGGCA TGGCGATTGGTACTGAGGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACCTCCGTC

2966 ESP1, 2969 SACI,

GluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSer 3002 GAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGACTCC CTCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTTTGTTTCACCACTAAGACCTGAGG

PheAspProLeuValAlaGluGluAspGluArgGluTleSerValProAlaGluTleLeu 3062 TTCGATCCGCTTGTGGCGGAGGAGGACGGGAGATCTCCGTACCCGCAGAAATCCTG AAGCTAGGGGAACACCGCCTCCTCCTGCTCGCCCTCTAGAGGCATGGGCGTCTTTAGGAC

3096 BGL2.

ArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnPro
3122 CGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCCGTTTGGGCGCGGCCGGACTATAACCCC

#### 

- 1 HIND3, 24 NDEI, 52 SCAI.
- ProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyIleAsp 62 CCCTCTGGTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGATCGAT GGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCTAGCTA

116 CLAI,

- ProAsnIleArgThrGlyValArgThrIleThrThrGlySerProIleThrTyrSerThr
  CCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTACTCCACC
  GGATTGTAGTCCTGGCCCCACTCTGTTAATGGTGACCGTCGGGGTAGTGATGAGTGG
- TyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleIleCys
  182 TACGCAAGTTCCTGCCGACGCGGGGTGTGCTGGGGGGCGCTTATGACATAATAATTTTT
  ATGCCGTTCAAGGAACGGCTGCCGCCCACGAGCCCCCCGGAATACTGTATTATTAACAA
- AspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuAspGln
  GACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATTGGCACTGTCGTCACCAA
  CTGCTCACGGTGAGGTGCCTACGGTGTAGGTAGACCCGTAAACCGTGAAAGGACTGGTT
- - 303 ALWN1.
- ThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGlyGluIleProPhe
  ACTGTGCCCCATCCCAACATCAGAGAGGTTGCTTCTTCCACCACCGGGAGAGATCCCTTTT
  TGACACGGGGTAGGGTTGTAGCTCCTCCAACGAGACACGTGTGCTCTCTAGGGAAAA
- TyrGlyLysAlaIleProLeuGluValIleLysGlyClyArgHisLeuIlePheCysHis
  422 TACGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGGAGACATCTCATCTTCTGCAT
  ATGCCGTTCCGATAGGGGGGGCTTCATTAGTTCCCCCCCTGTGAGGTAGAAGACAGTA

Tyrilelyshlahrghlahlacyshrghlahladlyleudinhspcysthrhetleuval
TACATCAAGGCCCGGCAGCTGTCGAGCCGCAGGGCTCCAGGACTGCACCATGCTCGTG
ATGTAGTTCCGGGCCCGTCGGACAGCTCCCCAGGTCCTAACGTGGTACGACAC

4452 SMAI XMAI.

CysGlyAspAspLeuValValIleCysGluSerAlaGlyValGlnGluAspAlaAlaSer
TGTGGCGACGACTTAGTCGTTATTCTGTAAAGCGCGGGGGTCCAGGAGGAGCAGGAGCACCAGCTGGATCAGCAATAGACACTTGGGCCCCCAGGGTCTCTGTGGCGCCCAG

4508 DRD1, 4511 TTH3I,

- LeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspProProGln
  4562 CTGAGAGCCTTCACGGAGCCTATGACCAGGTACTCCGCCCCCCCTAGGAGCCCCCCACAA
  GACTCTCGGAAGTGCCTCCGATACTGGTGCATGAGGCGGGGGACCCCTCGGGGGGTGTT
- ProGluTyrAspLeuGluLeuIleThrSercysSerSerAsnValSerValAlaHisAsp
  4622 CCAGATACGACTTGGACCTCATAACATCATGCTCCTCCAACGTGTCAGTCGCCCACGAC
  GGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTGCACAGTCAGCGGGTGCTG

4637 SACI,

GlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAlaArgAla GGGCGTGGAAAGAGGGTCTACTACCTCACCCGTGACCCTACAACCCCCCTCGGAAGCT CCGCGACCTTTCTCCCAGATGATGAGTGGCACTGGGATGTTGGGGGAGCGCTCTCGA

4731 NRUI.

- AlattpGluThrAlaArgHisThrProValAsnSerTtpLeuGlyAsnIleIleMetPhe GCGTGGGAGACAGCACACACTCCAGTCAATTCCTGGCTAGGCAACATAATCATGTTT GCACCCTCTGTGTTCTGTGTGAGGTCAGTTAAGGACCGATCCGTTGTATTAGTACAAA
- AlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAla GCCCCCACACTGTGGGCAGGATGATACTGATGACCCATTTCTTTAGCGTCCTTATAGCC CGGGGTGTGACACCCGCTCCTACTATGACTACTGGTAAAGAAATCGCAGGAATATCGG

4806 PFLM1, 4807 DRA3,

AFGASPGINLEUGIUGINAIALEUASPCYSGLUILETYYGIYALSCYSTYSSEILEGIU
AGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGCCTGCTACTCCATAGAA
TCCCTGGTCGAACTTGTCCGGGACCTAACGCTCTTGATTGCCCCGGACCATGAGGTATCTT

4893 BGL2.

ProLeuAspleuProProlleIleGlnArgLeuHisGlyLeuSerAlaPheSerLeuHis 4922 CCACTGGATCTACCTCCAATCATTCAAGACTCCATGGCCTCAGCGCATTTTCACTCCAC GGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGGATTCGCTAAAAGTGAGGTG

4954 NCOI,

SerTyrSerProGlyGlulleAsnArgValAlaAlaCysLeuArgLysLeuGlyValPro 4982 AGTTACTCTCCAGGTGAATCAATAGGTGGCCGCATGCCTCAGAAACTTGGGGTACG TCAATGAGAGGTCCACTTTAGTTATCCCACCGGGGTACGGAGTCTTTTGAACCCATGGC

5015 SPHI, 5035 KPNI,

5449 APAI.

GlyWalArgAlaThrArgLysThrSerGluArgSerGlnProArgGlyArgArgGlnPro
GGTGTGGCGCGCGAGAGAAGACTTCCGAGCGTCGCAACCTCGAGGTAGACGTCAGCCT
CACACGCGCGCTGCTCTTTCTGAAGGCTCGCAGCGTTGGAGCTCCATCTGCAGTCGGA
CACACGCGCGCTGCTCTTTTCTGAAGGCTCGCAGCGTTGGAGCTCCATCTGCAGTCGGA

5467 BSSH2, 5478 XMNI, 5502 XHOI, 5511 AAT2,

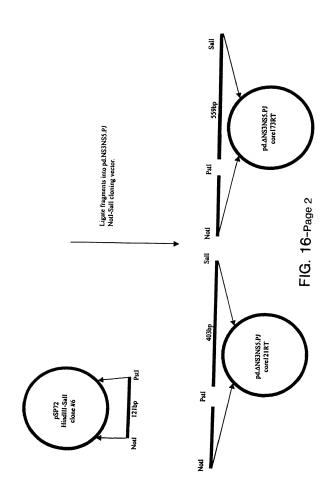
5548 ALWN1, 5558 ESP1, 5564 SMAI XMAI, 5568 KPNI,

- LeuTyrclyAsncluclyCysGlyTrpAlaGlyTrpLeuLeuSerFroArgGlySerArg
  CTCTATGCCAATGAGGCTGCGGGTGGGCGGGATGGCTCTGTCTCCCCTGGGCTCTCGG
  GAGATACCGTAGCTCCGAGGGCCACCGCCTACCGAGGACAAGGGGCAACGGAGACC

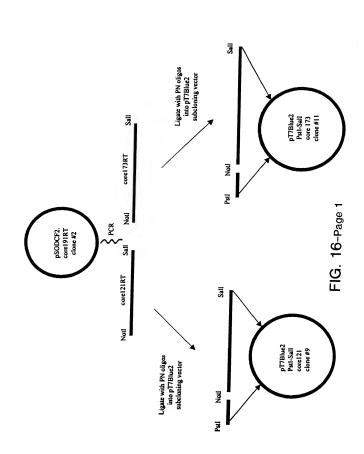
5650 APAI, 5698 SALI,

5702 AC TG

FIG. 17-Page 10



1322	4862	TCCCTGGTCGAACTTGTCCGGGAGCTAACGCTCTAGATGCCCCGGACGATGAGGTATCTT
		4893 BGL2,
1382	4922	ProLeuAspLeuProProIleIleGlnArgLeuHisGlyLeuSerAlaPheSerLeuHis CCACTGGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCACTCCAC GGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAAGTGAGGTG
		4954 NCOI,
1442	4982	SertyrserProGlyGluIleAsnArgValAlaAlaCysLeuArgLysLeuGlyValPro AGTTACTCTCCAGGTGAAATCAATAGGGTGCCCCATGCCTCAGAAAACTTGGGGTACCG TCAATGAGAGGTCCACTTTAGTTATCCCACCGGGGTACGGAGTCTTTTGAACCCCATGGC
		5015 SPHI, 5035 KPNI,
1502	5042	ProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGly CCCTTGCGAGCTTGGAGACACCGGGCCCGGAGCGTCCGCGGTAGGCTTCTGGCCAGAGGA GGGAACGCTCGAACCTCTGTGGCCCGGGCCCTGCAGGCGCGATCCGAAGACCGGTCTCCT
		5064 APAI, 5091 BALI,
1562	5102	GlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLys GGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAAGCTCAAA CCGTCCCGACGGTATACACCGTTCATGGAGAAGTTGACCCGTCATTCTTGTTTCGACTTT
		5113 NDEI,
1622	5162	LeuThrProlleAlaAlaAlaGlgGlnLeuAspLeuSerGlyTrpPheThrAlaGlyTyr CTCACTCCAATAGCGGCCGGTGGCCAGCTGGACTGGTCAGGGTGGCTAG GAGTGAGGTTATCGCCGGCGACCGGTCGACCTGAACAGGCCGACCAAGTGCCGACCGA
		5174 NOTI, 5175 EAG1 XMA3, 5182 BALI, 5186 PVU2,
1682	5222	SerGlyGlyAsplleTyrHisSerValSerHisAlaArgProArgTrpIleTrpPheCys AGCGGGGGAGACATTTATCACAGCGTGTCTCATGCCCGGCCCCGCTGGATCTGGTTTTCC TCGCCCCCTCTGTAAATAGTGTCGCACAGAGTACGGGCCGGGCGGACCTAGACCAAAACG
1742		5240 DRA3,
	5282	LeuLeuLeuLeuAlaAlaGlyValGlyIleTyrLeuLeuProAsnArgMetSerThrAsn CTACTCCTGCTGCGGGGGTAGGCATCTACCTCCTCCCCAACGGATGAGCAGAT GATGAGGACGAACGACGTCCCCATCCGTAGATGGAGGAGGGTTGGCTTACTCGTGCTTA
1802		5295 PSTI,
	5342	ProLysProGlnArgLysThrLysArgAsnThrAsnArgArgProGlnAspVallysPhe CCTAAACCTCAAAGAAAGACCAAACGTAACACCAACCGGCGGCGCAGAGACGTCAAGTTC GGATTTGGAGTTTCTTCTGGTTTGCATTGTGGTTGGCGCCGGCGTCCTGCAGTTCAAG
1862		5380 NOTI, 5381 EAG1 XMA3, 5390 AAT2, 5401 SMAI XMAI,
	3402	ProGlyGlyGlyGlnIleValGlyGlyValTyrLeuLeuProArgArgGlyProArgLeu CCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGGCCCTAGATTG GGCCCACCGCCAGTCTAGCAACCACCTCAAATGAACAACGGCGGTCCCCCGGGATCTAAC



4229 DRD1, 4236 ALWN1,

GluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIleLysSer 4262 GAGGAGGCAATCTACCAATGTTCTGACCCTCGACCCCGAGCCCGGGGGCATCAAGTCC CTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCGGGCCACCGGTAGTTCAG

4301 BGLI, 4308 BALI,

LeuthrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGly
4322 CTCACCGAAGGCTTTATGTGGGGCCCCTCTTACCAATCCAAGGGGGAGAACTGCGGC
GAGTGGCTCTCGAAATACAACCCCCGGGAGAATGGTAAGTCCCCCCTCTTGACGCCG

4345 APAI,

TyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCys
4382 TATGCGGGGGGGGGGGGGGAGGGGGTACTGACTAGCTGGTGAACACCCTCACTTGC
ATAGCGTCCACGGGGGGGGGTGCGCGCATGACTGTTGATCGACACCATTGTGGGAGTGAAC

Tyrllelysalargalahlacysargalahlaciyleuginaspcysthrmetleuval 4442 TACATCAGGCCCGGCACCCTGTCGAGCCGCAGGCTCCAGGACTGCACCATCCTCGTG ATGTAGTTCCGGGCCCGTCGGACAGCTCGGCGTCCGAGGTCCTGACGTGGTACGAGCAC

4452 SMAI XMAI,

CysGlyAspAspLeuValValIleCysGluSerAlaGlyValGlnGluAspAlaAlaSer 1502 TGTGGGGAGCTTAGTGTTAAAGGGCGGGGGTCCAGGAGGAGGAGGAGGAGAGAAGGACGCGGGAGA AACCGCTGCTGAATCAGCAATAGACATTGGGGCCCCAAGTCCTCCTGGGCCCTCG

4508 DRD1, 4511 TTH31,

ProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAlaHisAsp 4622 CCAGAATAGCACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTCAGTCGCCCACGAC GGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTGCACAGTCAGCGGTGCTG

4637 SACI,

GJyAlaGJyLyskrgValTyrTyrLeuThrArgAspFroThrThrProLeuAlaArgAla 4682 GGCCTTGGAAAGAGGTCTACTACCTCACCCGTGACCCTACAACCCCCCTCGGAGAGC CCGCGACCTTTCTCCCAGATGATGGAGTGGCACTGGGATGTTGGGGGGAGCCTTTCGA

4731 NRUI.

AlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAla 4802 GCCCCACACTGTGGGCAGGATGATACTGATGACCCATTTCTTTAGCGTCCTTATAGCC CGGGGTGTGACCGCTCCTACTATGACTACTGGTAAAGAAATCGCAGGAATATCG

4806 PFLM1, 4807 DRA3,

ArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGlu

3589 DRA3, 3600 SAC2,

AlaglugingintysleuproileAsnAlaLeuSerAsnSerLeuLeuArgHisHisAsn
GCGGAAGAACAGAAACTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTCACGAAAA
CGCCTTCTTGTCTTTGACGGGTAGTTACGTGATTCGTTGAGCAACGATGCAGTGGTGTTA

3611 ALWN1, 3655 PFLM1,

LeuWalTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThrPheAsp TTGGTGTATTCCACCACCTCACGCACTGCTTCCCAAAGGCAGAAAGTCACATTTGAC AACCACATAAGGTGGTGGAGTGGCTCACGAACGGTTTCCGTCTTCTTTCAGTGTAAACTG

3681 DRA3.

- ArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAlaAlaAla
  3722 AGACTGCAAGTTCTGGACAGCCATTACAGCAGCTTAAAGCAGCGGCG
  TCTGACGTTCAAGACCTGTCAGTAATGGTCCTGCATGCTTCCTCCCAATTTCGTCCCCGC
- SerLysVallysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrProProHis
  TCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCAGCCTGACGCCCCACAC
  AGTTTTCACTTCCGATTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGGGGTGTG

3816 HIND3,

3875 AAT2, 3890 BGLI,

- ValThrHis1leAsnSerValTrpLysAspLeuLeuGluAspAsnValThrProIleAsp GTAACCCACATCAACTCCGTGTGGAAGACCTTCTGGAAGACATGTAACACCCAATAGAC CATTGGGTGTAGTGAGGCAACCTTTCTGGAAGACCTTCTGTACATTGGTTATCTG
- ThrThrIeMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGlyArgLys
  ACTACCATCATGGCTAAGAACGAGGTTTTTCTGCTTCAGCCTGAGAAGGGGGGTCCTAAG
  TGATGGTAGTACCGATTCTTGCTCCAAAAGACGGAAGTCGGACTCTTCCCCCAGCATTC
- ProAlaArgLeuilevalPheProAspLeuGlyValArgValCysGluLysMetAlaLeu CCAGCTCGTCTCATCGTGTTCCCCGATCTGGGCGTGGGGAAAAGATGGCTTTG GGTGGACAGAGTAGCACAGGGGTAGACCGCACGCGACGCACACGCTTTTACCGAAAC
- TYRASPValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPheGlnTyr TACGACGTGGTTACAAAGCTCCCCTTGCGCGTGATGGGAAGCTCCTAAGAG ATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCCTTCGAGGATTCCTAAGGTTATG
- SerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThrProMet 1422 TCACCAGGACAGCGGTTGAATTCCTGTGCAAGCGTGGAAGTCCAAGAAAACCCCCAATG AGTGGTCCTGTCGCCCAACTTAAGGAGCACGTTCGCACCTTCAGGTTCTTTTGGGTTAC

4160 ECORI,

GlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIleArgThr 4202 GGGTTCTCGTATACCCCCTGCTTTGACTCCACAGTCACTGAGAGGGACATCCGTAGG CCCAAGAGCATACTATGGGCGACGAAACTGAGGTGTCAGTGACTCTCGCTGTAGGGATGC

2942	ThralaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGln ACGGCTAACCATGACTCCCCTGATGCTGAGGCTCATAGAGGCCAACCTCCTATGGAGGCAGTGGCGATTGGTACTGAGGGATACCTCCGTCTGAGGATTACTCCGGTTGGAGGATACCTCCGTC
3002	2966 ESP1, 2969 SACI, GluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSer GAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGACTCC CTCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTTTGTTTCACCACTAAGACCTGAGG
3062	PheAspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGluIleLeu TTGGATCCGCTTGTGGCGGAGGAGGACGAGCGGGAGATCTCCGTACCCGCAGAAATCCTG AAGCTAGGCGAACACCGCCTCCTCCTGCTCGCCCTCTAGAGGCATGGGCGTCTTTAGGAC
	3096 BGL2,

 ${\tt ArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnPro}$ 3122 CGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCCGTTTGGGCGCGGGCCGGACTATAACCCC GCCTTCAGAGCCTCTAAGCGGGTCCGGGACGGGCAAACCCGCGCCGGCCTGATATTGGGG

3143 ALWN1, 3164 EAG1 XMA3.

ProLeuValGluThrTrpLysLysProAspTyrGluProProValValHisGlyCysPro 3182 CCGCTAGTGGAGACGTGGAAAAAGCCCGACTACGAACCACCTGTGGTCCATGGCTGCCCG GGCGATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGACACCAGGTACCGACGGGC

3217 HGIE2, 3229 NCOT.

- LeuProProProLysSerProProValProProProArgLysLysArgThrValValLeu 3242 CTTCCACCTCCAAAGTCCCCTCCTGTGCCTCCGCCTCGGAAGAAGCGGACGGTGGTCCTC GAAGGTGGAGGTTTCAGGGGAGGACACGGAGGCGGAGCCTTCTTCGCCTGCCACCAGGAG
- 3302 ACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGCAGCTCC TGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAAACCGTCGAGG

3332 SACI, 3346 HIND3,

- SerThrSerGlyIleThrGlyAspAsnThrThrThrSerSerGluProAlaProSerGly 3362
- CysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGlyGluPro TGCCCCCCGACTCCGACGCTGAGTCCTATTCCTCCATGCCCCCCCTGGAGGGGGAGCCT 3422 ACGGGGGGGGCTGAGGCTCAGGATAAGGAGGTACGGGGGGGACCTCCCCCTCGGA

3437 EAM11051.

GlyAspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsnAlaGlu 3482 GGGGATCCGGATCTTAGCGACGGGTCATGGTCAACGGTCAGTGAGGCCAACGCGGAG CCCCTAGGCCTAGAATCGCTGCCCAGTACCAGTTGCCAGTCATCACTCCGGTTGCGCCTC

3484 BAMHI, 3485 BSAB1, 3487 BSPE1,

3542 GATGTCGTGTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCGTGCGCC CTACAGCACACGAGTTACAGAATGAGAACCTGTCCGCGTGAGCAGTGGGGCACGCGG

# FIG. 17-Page 6



FIG. 15

- 662 ACGTGTGTCACCCAGACAGTCGATTTCAGCCTTGACCCTACCTTCACCATTGAGACAATC
  TGCACACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGGATGGAAGTGGTAACTCTGTTAG
- ThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLys
  722 ACGCTCCCCAAGATGCTGCTCCCCGCACTCAACGTGGGGCAGGACTGCCAGGGGAAG
  TGCGAGGGGGTTCTACGACAGAGGGCGTGACTTGCAGCCCGTCCTGACCGTCCCCTTC
- ProGJylleTyrArgPheValAlaFroGlyGluArgProSerGlyMetPheAspSerSer
  782 CCAGGCATCTACAGATTTGGCACCGGGGGAGGCCCCCCCGGGATGTTCGACTCGTC
  GGTCCGTAGATGTCTAAACACCGTGGCCCCTCGCGGGAGGCCCTACAAGCTGAGCAG

816 BGLI, 833 DRD1.

881 SACI,

ThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAspHisLeu
902 ACAGTTAGGCTACGAGGGTACATGACACCCGGGGGCTTCCCGTGTGCAGGACCATCTT
TGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCTCTGTAGAA

931 SMAI XMAI.

GluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGln 962 GAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGAGTCCCACTTTCTATCCCAG CTTAAAACCCTCCGCAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAAGTAGGGTG

985 STUI.

ThrLysGlnSerGlyGluAsnLeuProTyrLeuVallaTyrGlnAlaThrValCysAla
ACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGGT
TGTTTCGTCTCACCCCTCTTGGAAGGAATGGACTGCATGGTTCGGTGGTTCGGTGGACACGGGA

1069 DRA3.

- ArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeuLys
  1082 AGGGCTCAAGCCCCTCCCCATCGTGGGACGAGTATGGAAGTGTTTGATTCGCCTCAAG
  TCCCGAGTTCGGGGAGGGGGTAGCACCCTGGTCTACACCTTACAAACTAAAGGGAGTTC

1150 NCOI,

1230 BSPH1, 1234 DRD1, 1237 AVA3, 1245 EAG1 XMA3, 1250 DRD1,

5042	CCCTTGCGAGCTTGGAGACACCGGGCCCGGAGCGTCCGCGCTAGGCTTCTGGCCAGAGGA
	GGGAACGCTCGAACCTCTGTGGCCCGGGCCTCGCAGGCGCGATCCGAAGACCGGTCTCCT

5064 APAI, 5091 BALI,

GlyArgAlaAlaTleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLys 5102 GGCAGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAAAAGCTCAAA CCGTCCCGACGGTATACACCGTTCATGGAGAAGTTGACCCTCATCTTCTTTCGAGTTT

5113 NDEI.

LeuThrProfleAlaAlaAlaGlyGlnLeuAspLeuSerGlyTrpPheThrAlaGlyTyr
CTCACTCCAATAGCGGCGGGCGGGGGAGCTGGTCGGCGGGTGGTTACGGGTGGCTAC
GAGTGAGGTTATCGCCGGCGACCGGTGGACTGACCGACCAAGTGCGACCAAGTGCGACCAAGTGAGGTGACGGGTGACGACGACGACGACGACGACGACG

5174 NOTI, 5175 EAG1 XMA3, 5182 BALI, 5186 PVU2,

SerGlyGlyAspIleTyrHisSerValSerHisAlaArgProArgTrpIleTrpPheCys 5222 AGCGGGGGACATTTATCACACCGTGTCTCTATCCCGGCCCCGGTGGATCTGGTTTTGC TCGCCCCCTCTGTAAATAGTGTGCACAGAGTACGGGCCGGGGGACCTAGACCAAAACG

5240 DRA3,

LeuLeuLeuLeuAlaAlaGlyValGlyTleTyrLeuLeuProAsnArgoP
5282 CTACTCCTGCTGCAGGGGTAGGCATCTACCTCCCCACCGATGAATAGTCGAC
GATGAGGACGAACGACGTCCCCATCCGTAGATGGAGGAGGGGTTGGCTACTTATCAGCTG

5295 PSTI, 5336 SALI,

FIG. 14-Page 9

TyrIIeLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMetLeuVal
TACATCAAGGCCCGGCAGCCTGTCGAGCCGCAGGGCTCCAGGACTGCACCATGCTCGTG
ATGTAGTTCCGGCCCCTGCGACACGCCCCGAGGTCCTGACGTGGTACGACCAGCAC
4452 SMAI XMAI,
CysGlyAspAspLeuValValIleCysGluSerAlaGlyValGlnGluAspAlaAlaSer
TGTGGCGACGACTAGTCGTTATCTGTGAAAGCCCGGGGGTCCAGGAGGACGCGCGAGC
ACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCCAGGTCCTCCTGCCGCCGCTCG
4508 DRD1, 4511 TTH31,

ProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAlaHisAsp 4622 CCAGAATACGACTTGGAGCTCATAACATCATCCTCCTCCAACGTGTCAGTCGCCCACGAC GGTCTTATGCTGAACCTCGAGTATTGTAGTAGGAGGAGGTGCACATGAACGGGGTGTTG

4637 SACI.

4731 NRUI.

AlatrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMetPhe
GGGTGGGAGACAGCAACACTCCAGTCAATTCCTGGCTAGGCAACATAATCATGTTT
CGGACCCTCTGTCGTTCTGGTGAGGTCAGTTAGGACCATCCGTTCGATTATTATAACAAA

AlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAla
GCCCCCACACTGTGGGCAAGATGATACTGATGACCCATTTCTTTAGCGTCCTTATAGCC
CGGGGTGTGACACCCGCTCCTACTATGACTACTGGGTAAAGAAATCGCAGGAATATCGG

4806 PFLM1, 4807 DRA3,

ArgAspGinLeuGluGinAlaLeuAspCysGluTleTyrGlyAlaCysTyrSerIleGlu AGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACCATAGAA TCCCTGGTCGAACTTGTCCGGGAGCTAACGCTCTAGATGCCCCGGACGATGAGGTATCTT

4893 BGL2.

ProLeuAspleuProProllelleGlnArgLeuHisolyLeuSerAlaPheSerLeuHis CCACTGGATCTACCTCCAATCATTCAAGACTCCATGGCCTCAGCGCATTTCCACTCCAC GGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAAGTGAGGTG

4954 NCOI.

SerTyTSerProGlyGluIleAsnArgValAlaAlaCysLeuArgLysLeuGlyValPro 4982 AGTTACCTCCCAGGTGAATCAATAGGGTGGCCCCATGCCTCAGAAAACTTGGGGTACCG TCAATGAGAGGTCCACTTTAGTTATCCCACCGGCGTACGGAGTCTTTTGAACCCCATGGC

5015 SPHI, 5035 KPNI.

 ${\tt ProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGly}$ 

1884 SACI, 1905 BSPH1,

ProSerThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuVal
1922 CCCTCCACGGAGGACCTGCTAATCTACTGCCGCCACTCCTCTCCCCGGAGCCCTCGTA
GGGAGGTGCCTCCTGGACCAGTTAGATGACGGGCGTTAGGAGAGCGGGGCCTCGGGAGCAT

1934 TTH3I.

2010 NAEI, 2023 SMAI XMAI.

GINTIPMENASARIGLEUILEALAPHEALASERARGGIYASHHISVAISERPROTHRHIS
CAGTGGATGAACCGGCTGATAGCCTTCSCCTCCCGGGGGAACCATGTTTCCCCCAGGCAC
GTCACCTACTTGGCCGACTATCGGAAGCGGAGGCCCCCTTGGTACAAAGGGGGGGTCCTG

2073 SMAI XMAI, 2099 DRA3,

TYTVALPROGIUSERASPALAALAALAATGVALTHRALATLELEUSERSERLEUTHRVAL 2102 TAGCTGCCGGAGAGCGATGCAGCCGCGCACTCCACTACCAGCAGCCTCACTGTA ATGCACGGCCTCTCGCTCGACGGGCGCAGTTACGGTATGAGTGCTATGAGTGCACTGAGTGCACT

2121 PVU2,

ThrGinLeuLeuArgArgLeuHisGinTrpIleSerSerGluCysThrThrProCysSer
2162 ACCAGCTCCTGAGGCGACTGCACCAGTGATAGGTCGAGTGTACCACTCCATGCTCC
TGGGTCGAGGACTCCGCTGACGTTGACCTATTCGAGCCTCAATGGTGAGGTACGAGG
TGGGTCGAGGACTCCGCTGACGTTGACCTATTCGAGCCTCAA

2165 ALWN1, 2170 MST2.

GlySerTrpLeuArgAsplleTrpAspTrpIleCysGluValLeuSerAspPheLysThr GGTTCCTGGCTAAGGGACTGTGGACTGGATATGCGAGGGTCTTGAGGGAC CCAAGGACCGATTCCCTGTAGACCTGACCATATACGCTCCACAACTCGCTGAAATTCTGG

2226 ECON1,

TTPLeuLysklalysLeuMetProGinLeuProGlylleProPheValSerCysGinArg
TGGCTAAAAGCTAAGCTCAGGCGCGCCTGGGATCCCCTTTGTGTCCTGCCAGGGC
ACCGATTTTCGATTAGGTGTCTGACGAGCCCTAGGGAAACACAGGAGGGTCGCG

2291 ESP1, 2306 PVU2, 2316 BAMHI,

- GlyTyrLysGlyValTrpArgGlyAspGlyIleMetHisThrArgCysHisCysGlyAla 2342 GGGTATAAGGGGTCTGCCGAGGGGAGGGATCATGGACACTCGCTGCACTTGGAGCT CCCATATTCCCCCAGACCGCTCCCCTGCCGTAGTACGTGTGAGCGACGGGACACTCTGA
- GLUIIeThrGlyRisValLysAsnGlyThrMetArgIleValGlyFroArgThrCysArg
  GAGATCACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCCTAGGACCTCCAGG
  CTCTAGTGACCTGTACAGTTTTGCCTTGCTAGTCTCTAGCGTGCC

2431 BSAB1, 2447 AVR2, 2454 SSE83871, 2455 PSTI,

ARMMetTipSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeu
AACATGTGGAGTGGGACCTTCCCCATTAATGCCTACCCCCCTGTACCCCCCTT
TTGTACACCTACCCCTTGGAGGGGTAATTACGGTGTGTGCCCGGGGACTTGGGGGGAA

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- 1 HIND3, 24 NDEI, 52 SCAI,
- ProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLySAlaHisGlyIleAsp
  CCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGATCGAT
  GGGAGACAACGACGTTGTGACCCGAAACCACGATGTACACGTTCCCAGTACCCTAGCTA
  - 116 CLAI.
- ProAsnIleArgThrGlyValArgThrIleThrThrGlySerProIleThrTyrSerThr 122 CCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCAGGTACTCCACC GGATTGTAGTCCTGGCCCCACTCTGTTAATGGTGACCGTCGGGGTAGTGATGAGGTG
- TyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleIleCys
  182 TACGCAAGTTCCTTGCCGACGGCGGGTGCTCGGGGGGCCTTATGACTAATAATTTGT
  ATGCCGTTCAAGGAACGGCTGCCGCCCACGAGCCCCCCGGATAACTGATTATTAATAACA
- AspGluCysHisSerThrAspAlaThrSerTleLeuGlyIleGlyThrValLeuAspGln
  242 GACGAGTGCCACTCCACGGATGCCACATCATCATCTTGGGCATTGGCATGGCATGTGCTTAACCATCTCTGACCAA
  CTGCTCACGGTGAGGTGCCTACGGTGTAGGTGAACCGGTAACCGTGAACGGAACTGGTT
- AlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrProProGlySerVal
  302 GCAGAGACTGCGGGGGGGACTGGTTGTGCTCGCCACCGCCACCCCTCCGGGCTCGTC
  CCTCTCTGACCCCCCCCTCTGACCAACACGAGCGGTGGCGTGGGAGGCCCGAGCAG
  - 303 ALWN1,
- ThrValProHisProAsnIleGluGluValAlaLeuserThrThrGlyGluIleProPhe
  362 ACTGTGCCCCATCCCAACATCGAGGAGGTGCTTCTTCTCCACCACCGGGAGAGATCCCTTTT
  TGACACGGGGTAGGGTTGTAGCTCCTCCAACGAGACACGTGGCCTTCTTAGGGAAAA
- TyrGlyLysAlaileProLeuGluValTieLysGlyGlyArgHisLeuIlePheCysHis
  422 TACGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGGAGACATCTCATCTTCTCATA
  ATGCCGTTCCGATAGGGGAGCTTCATTAGTTCCCCCCCTGTAGAGTAGAGACAGTA
- SerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGly11eAsnAlaVal
  182 TCAAAGAGAAGTGCGAACTGCGCGCAAAGCTGGTGCATTGGGATCAATGCCGTG
  AGTTTCTTCATCAGGCTGCTTGAGGGGGGTTTCGACCAGTAACCCGTAACCCGTATTGAGGCA
- - 550 SAC2, 560 DRD1,
- AlathraspalaLeuMethrclyTyrThrClyAspPheAspSerValILeAspcysAsn 602 GCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGCTCCAAT CCTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCACCTATGTCTGACGTTA
  - 615 BSPH1.

 $Thr {\tt CysValThr GlnThr Val AspPhe Ser Leu AspProThr Phe Thr {\tt IleGluThr IleGluThr$ 

1322	CysLeuSerThrGlyCysValValIleValGlyArgValValLeuSerGlyLysProAla TGCCTGTCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTGTCCGGGAAGCCGGCA ACGGACAGTTGTCCGACGCACCAGTATCACCCGTCCCAGCAGAACAGGCCCTTCGGCCGT
	1375 NAEI,
1382	IleIleProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGln ATCATACCTGACAGGAAGTCCTCTACCGAGAGTTCGATGGAGAGAGTGCTCTCAG TAGTATGGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTACCTTCTCACGAGAGTC
	1391 DRD1,
1442	HisLeuProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeu CACTTACCGTACATCGAGCAGGGATGATGCTCGCCGAGCAGTTCAAGCAGGAGGCCCTC GTGAATGGCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCCCGGAG

1508 PSTI, 1513 TTH3I,

TFGGInLysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGlyIleGIn 1562 TGGCAAAAACTCGAGACCTTCTGGGGAAGCATATGTGGAACTTCATCAGTGGGATACAA ACCGTTTTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAGTATACCCCTATGTT

1571 XHOI, 1592 NDEI,

TyrLeuAlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPhe
1622 TACTGGGGGGCTTGTCAAGGCTGCCTGGTAACCCATTCCTTCATTGATGGCTTTT
ATGAACCGCCCGAACAGTTGCGACGGACCATTGGGGGGGTAACGAAGTAACTACCGAAAA

1649 BSTE2,

ThrAlaAlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGly
ACAGCTGCTGTCACCAGCCCACTACCACTAGCCAAACCCTCCTCTTCAACATATTGGGG
TGTCGACGACGAGTGGTCGGGTGATTGGTGATCGGTTTGGGAGGAGAAGTTTATTAACCCC

1683 ALWN1 PVU2.

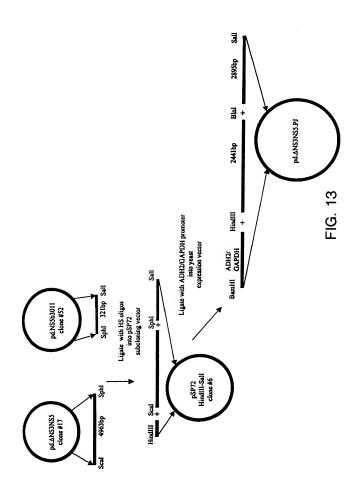
GLYTTPVAIALaALaGInLeuAlaALaProGlyAlaAlaThrAlaPheValGlyAlaGly
1742 GGGTGGGTGCCCCACCCCCGGTGCCCCTACTGCCTTTGTGGCGCTGCC
CCCACCCACCGACGGGTGGACGCACACCACCGCACACG
CCCACCCACCGACGGGTGAGCGAAACACCGCCACCG

1800 ESP1,

LeuhlaciyAlahlailaciySerValciyLeuGiyLysValLeuIleAspileLeuhla TTAGCTGGCGCCGCATCGCAGCTGTGGACTGGGGAAGGTCCTGATAGACATCCTTGCA AATCGACCGCGGCGGTAGCCGTCACAACCTGACCCCTTCCAGGAGTATCTGAGGAGGT

1808 KAS1 NARI.

GIYTYrG1yAlaG1yValAlaG1yAlaLeuValAlaPheLysIleMetSerG1yG1uVal 1862 GGGTATGGCGCGGGGGGGCCTCTTGTGGCATTCAAGATCATGAGCGGTAGGGTC CCCATACCGCGCCCCCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTGCCACTCCAG



- 662 TGCAATACGTGTGTCACCCAGACAGTCGATTTCAGCCTTGACCCTACCTTCACCATTGAG
  ACGTTATGCACACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGGATGGAAGTGGTAACTC
- ThrIIeThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArg
  ACAATCACGCTCCCCCAAGATGCTGTCTCCCGCACTCAACGTCGGGGAGGACTGCAGG
  TGTTAGTGCGAGGGGTTCTACGACAGAGGGCGTGAGTTCCAGCCCCCTCTGACCTTCC
- GlyLyeFroGlyIleTyrArgPheValAlaFroGlyGluArgProSerGlyMetPheAsp 782 GGGAAGCCAGGCATCTACAGATTTGTGGCACCGGGGGGAGGCCCCCTCGGCATGTTCGAC CCCTTCGGTCGTAGATGTCTAAACACCGTGGCCCCCTCGGGGGAGGCGTACAAGCTG
  - 822 BGLI, 839 DRD1.
- SerSerValLeuCysGlucysTyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAla
  142 TCGTCCGTCCTCTGGAGTGCTATGACCAGGCTGTGCTTGGTATAGCTCAGGGCGCC
  AGCAGGCAGGAGCATCACGATACTGGGTCCGACGAACCATACTGAGTGCGGGGGG
  - 887 SACI,
- GluthrThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAsp 902 GAGACTACAGTTAGGCTACGAGGCGTACATGAACACCCCGGGGCTTCCCCGTGTGCCCAGGAC CTCTGATGTCAATCCGATGCTGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCCTG
  - 937 SMAI XMAI,
- - 991 STUI.
- SerGinthrLysGinSerGlyGluAsnLeuProTyrLeuValAiaTyrGinAiaThrVal
  1022 TCCCAGACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGCAC
  AGGGTCTGTTTCGTCTCACCCTCTTGGAAGGAATGACCATCGCATGGTTCGGTGGCAC
  - 1075 DRA3,
- CysAlaArgAlaGinAlaProProProSerTrpAspGinMetTrpLysCysLeuIleArg
  1082 TGCGCTAGGGCTCAAGCCCCCTCCCCCATCGTGGGACAGATGTGGAAGTGTTTGATTCGC
  ACGGGATCCCGAGTTCGGGGAGGGGTAGCACCTTGATCTACACCTTCACAAACTAAGC
- LeuLysProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsn
  1142 CTCAAGCCCACCTCCATGGGCCAACACCCTTGCTATACAGACTGGGGGGTGTCAGAAT
  GAGTTGGGGGGGAGTACCGGTTGTGGGGACGATATGTCTGACCGGCACAAGTTA
  - 1156 NCOI,
- - 1236 BSPH1, 1240 DRD1, 1243 AVA3, 1251 EAG1 XMA3, 1256 DRD1,
- GluValValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyr
  GAGGTCGTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTTGGCCGCGTAT
  CTCCAGCAGTGCTCGTGGACCCACGAGCAACCGCGCAGAACCGAAACCGGCGCATA

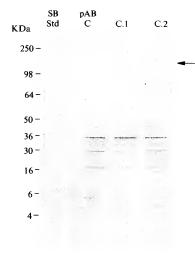


FIG. 12

3782	SerLysVallysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrProProHis TCAAAACTGAAGGCTAACTTGCTATCCGTAGAGGGAAGCTTGCAGCCCTGACGCCCCCACAC AGTTTTCACTTCCGATTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGGGGTGTG
	3816 HIND3,
3842	SerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArgLysAla TCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACCTCCGTTGCCATGCCAGAAAGGCC AGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCTTTCCGG
	3875 AAT2, 3890 BGLI,
3902	ValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrProlleAsp GTAACCCACATCAACTCCGTGGGAAAGACCTTCTGGAAGACAATGTAACACCAATAGAC CATTGGGTTGAGTTGA
	ThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGlyArgLys

- 3962 ACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGGTTGTAAG TGATGGTAGTACCGATTCTTGCTCCAAAAGACGCAAGTCGGACTCTTCCCCCCAGCATTC
- PFOAlaArgLeulleValPheProAspLeuGLyValArgValCysGluLysMetAlaLeu
  4022 CAGGCTGGTCTCATGGTGTTCCCCGATCTGGGCGTGGGGCACACGGTTTTCTACGCAAAC
  GGTCGACCAGAGTAGCACAGGGGCTAGACCCGCACACGGACACGCTTTTCTACCGAAAC
- TyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPheGlnTyr
  TACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCTCCTACGGATTCCAATAC
  ATGCTGCACCAATGTTTCGAGGGAACCGCACTACCCTTCGAGGATGCCTAAGGTTATG
- SerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThrProMet
  TCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACCCCAATG
  AGTGGTCCTGTCGCCCAACTTAAGGAGCACGTTCGCACCTTCAGGTTCTTTTTGGGGTTAC
  - 4160 ECORT.
- GlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIleArgThr GGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCGTACG CCCAAGAGCATACTATGGGCACGAAACTGAGGTTCAGTGACTCTCCCTGTAGGCATGC
  - 4229 DRD1, 4236 ALWN1,
- GluGluAlaIleTyrGlnCysCysAspLeuAepProGlnAlaArgValAlaIleLysSer GAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAGCCCGCGTGGCCATCAAGTCC CTCCTCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCGGGCCACCGGTAGTTCAGG
  - 4301 BGLI, 4308 BALI,
- LeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGly
  GTCACCGAGAGGCTTTATGTGGGGCCCTCTTACCATTCAAGGGGGAGAACTCCGGC
  GAGTGGCTCTCCGAAATACAACCCCCGGGAGAATGGTTAAGTTCCCCCTTTAGAGCCG
  - 4345 APAI,
- TYPARGATGCYSARGALSSERGLYVALLEUTHTTHTSSERCYSGLYASHTHTLEUTHTCYS
  TATCGCAGGTGCCGCGCGAGCGGCGTACTGACAACTGGTGTGTAACACCCTCACTTGC
  ATACCGTCCACGGCCGCTCCCGCATGACTGTTGATCGACACCATTGTGGAGGTGAAGA

GCCTTCAGAGCCTCTAAGCGGGTCCGGGACGGGCAAACCCGCGCCGGCCTGATATTGGGG

3143 ALWN1, 3164 EAG1 XMA3,

ProLeuValGluThrTTpLysLysProAspTyrGluProProValValHisGlyCysPro
3182 CCGCTAGTGGAGACGTGGAAAAAGCCCGACTACGAACCACCTGTGGTCCATGGCTGCCG
GGCGATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGACACCAGGTACCGACGGC

3217 HGIE2, 3229 NCOI,

- LeuproProProLysSerProProValProProProArgLysLysArgThrValValLeu CTTCCAACTCCAAAGTCCCCTCCTGTGCCTCCGGCTCCGGAAGAAGCAGCGGACGGTCGTCCTC GAAGGTGGAGGTTTCAGGGGAGGACACGGAGGCGGAGCCTTCTTCCCCTGCCACCAGGAG
- ThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGlySerSer
  3302 ACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGCAGCTCC
  TGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGTTGTTCTTCCAAACCGTCGAG

3332 SACI, 3346 HIND3,

- CysProProAspSerAspAlaGluSerTyrSerSerMerProProLeuGluGlyGluPro
  1422 TGCCCCCCGACTCCGACGCTGAGTCCTATTCCTCCATGCCCCCCCTGGAGGGGGAGCCT
  ACGGGGGGCCTAAGGCTCAGGATAAGGAGTACGGGGGGACCTCCCCCTCCGA

3437 EAM11051,

GlyAspProAspLeuSerAspGlySerTrpSerThrVelSerSerGluAlasnAlaGlu
GGGGATCCGGATCTTAGCGACGGGTCATGGTCAACGGCTCAGTAGTGAGGCCAACGCGGAG
CCCCTAGGCCTAGGATCGCCAGTACCAGTTGCCAGTTATCACTCCGGTTCGCCCTC

3484 BAMHI, 3485 BSAB1, 3487 BSPE1,

AspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrProCysAla 3542 GATGTCGTGTGCTCAATGTCTTACTCTTGGACAGGGGCACTCGTCACCCCGTGCGC CTACAGCACAGACGAGTACAGAATGAGAAACTGTCCGGGTGAGCAGTGGGGCACGCG

3589 DRA3, 3600 SAC2,

AlaGluGluGlnLysLeuProlleAsnAlaLeuSerAsnSerLeuLeuArgHisHisAsn
GCGGAAGAACAGAAACTGCCCATCAATGCACTAAGCAACTGGTTGCTACGCACACAAT
GCCTTCTTGTCTTTGACGGGTAGTTACGTGATTCGTTCAGCAACGATGCAGTGGTGTTA

3611 ALWN1, 3655 PFLM1,

LeuWalTyrSerThrThrSerArgSerAlacysGlnArgGlnLysLysValThrPheAsp 3662 TTGGTGTATTCCACCACCTCACCCAGTGCTTGCCAAAGGCAGAAGAAGTCACATTTGAC AACCACATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGTCTTCTTTCAGTGTAAACTG

3681 DRA3,

ArgleuginvalleuaspserHistyrGinaspvalleuLysGluvalLysalaalaala
3722 AGACTGCAAGTTCTGGACAGCCATTACCAGGACTACTAAGGGTTAAAGAGCTGCAGCGGG
TCTGACGTTCAAGACCTGTCGGTAATGGTCCTGCATGAGTTCCTCCAATTCGTCGCCGC

ValProProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAla 5042 GTACCGCCCTTGCCAGCTTGGAGACACCGGGCCCGGAGGCTCGCGCAGAGCCTC CATGGCGGAACGCTCGAACCTCTGTGCCCGGGCCTCGCAGGCCGCATCCGAAGACCGC

5070 APAI, 5097 BALI,

ArgGlyGlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLys
5102 AGAGGAGGCAGGCCTGCCATATGTGGCAAGTACCTGTCAACTGCGCAGTAACAACAAAG
TCTCCTCCGTCCGAGCGTATACACCGTTCATGGAGAAGTAACTGACCGTTCATTCTTGTTTC

5119 NDEI,

LeulysLeuThrProIleAlaAlaAlaGlyGlnLeuAspLeuSerGlyTrpPheThrAla
5162 CTCAAACTCACTCCAATAGCGGCCGCTGGCCAGCTGGAACTGGGCGTGGTGACGGGT
GAGTTTGAGTGAGGTAGTTATCGCCGGCGACCGGTCGACCTGAACAGGCCGACCAAGTCCCGA

5180 NOTI, 5181 EAG1 XMA3, 5188 BALI, 5192 PVU2,

GlyTyrSerGlyGlyAsplleTyrHisSerValSerHisAlaArgProArgTrpIleTrp
5222 GCCTACAGCGGGGAGACATTTATCACAGCGTGTCTCATCCCCGCCCCGTGGATCTGG
CCGATGTCGCCCCCTTGTAAATAGTGTCGCACAGAGTACGGGCCGGGGCAGCCTGAGAC

5246 DRA3,

PheCysLeuLeuLeuLeuAlaAlaGlyValGlyIleTyrLeuLeuProAsnArgOP
TTTTGCCTACTGCTGCTGCAGGGGTAGGCATCTACCTCCTCCCCAACCGATGAAGG
AAAACGGATGAGGACGAACGACGTCCCCATCCGTAGATGGAGGAGGGGTTGGCTACTTCC

5301 PSTI, 5331 HGIE2,

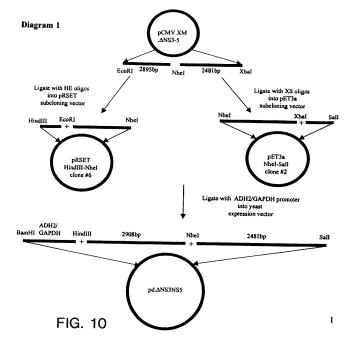
5378 XBAI, 5390 SALI,

FIG. 11-Page 9

#### MetAlaAlaTyrAlaAlaGlnGlyTyrLysVaILeuVal

- 2 AGCTTACAAAACAAATTCACCATGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTA TCGAATGTTTTGTTTAAGTGGTACCGACGTATACGTCGAGTCCCGATATTCCACGATCAT
  - 1 HIND3, 21 NCOI, 30 NDEI, 58 SCAI,
- LeuAsnProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGly 62 CTCAACCCCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGG GAGTTGGGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCC
- ${\tt IleAspProAsnIleArgThrGlyValArgThrIleThrThrGlySerProIleThrTyr}$ ATCGATCCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTAC TAGCTAGGATTGTAGTCCTGGCCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGCATG
  - 122 CLAI,
- $SerThrTyrGlyLysPheLeu \verb|AlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIle| \\$ AGGTGGATGCCGTTCAAGGAACGGCTGCCGCCCACGAGCCCCCCGCGAATACTGTATTAT
- ${\tt IleCysAspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeu}$ ATTTGTGACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATTGGCACTGTCCTT TAAACACTGCTCACGGTGAGGTGCCTACGGTGTAGGTAGAACCCGTAACCGTGACAGGAA
- AspGlnAlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrProProGly 302 GACCAAGCAGAGACTGCGGGGGCGAGACTGGTTGTGCTCGCCACCGCCACCCCTCCGGGC CTGGTTCGTCTCTGACGCCCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGGAGGCCCG
  - 309 ALWN1.
- SerValThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGlyGluIleTCCGTCACTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATC 362 AGGCAGTGACACGGGGTAGGGTTGTAGCTCCTCCAACGAGACAGGTGGTGGCCTCTCTAG
- ${\tt ProPheTyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeuIlePhe}$ 422 CCTTTTTACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGGAGACATCTCATCTTC GGAAAAATGCCGTTCCGATAGGGGGAGCTTCATTAGTTCCCCCCCTCTGTAGAGTAGAAG
- CysHisSerLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsn 482 TGTCATTCAAAGAAGAAGTGCGACGAACTCGCCGCAAAGCTGGTCGCATTGGGCATCAAT ACAGTAAGTTTCTTCTTCACGCTGCTTGAGCGGCGTTTCGACCAGCGTAACCCGTAGTTA
- AlaValAlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAspValVal 542 GCCGTGGCCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCAGCGGCGATGTTGTC CGGCACCGGATGATGGCGCCAGAACTGCACAGGCAGTAGGGCTGGTCGCCGCTACAACAG
  - 556 SAC2, 566 DRD1,
- ValValAlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerValIleAsp GTCGTGGCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGAC CAGCACCGTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTG
  - 621 BSPH1.

 ${ t CysAsnThrCysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGlu}$ 



ACGCCGATAGCGTCCACGGCGCGCTCGCCGCATGACTGTTGATCGACACCATTGTGGGAG

ThrCysTyr11eLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMet 4442 ACTGCTACATCAAGGCCCGGCAGCCCTTGCAGCGCAGGGGTCCAGGACTGCACCATG TGAACGATGTACTTCCGGCCCCTGGACAGCTGGGGTCCCGAGGTCCTAAGGTGTTAC

4458 SMAI XMAI.

LeuValCysGlyAspAspLeuValValIleCysGluSerAlaGlyValGinGluAspAla 4502 CTCGTGTGTGGCACGACTTAGTCGTTAATCTGTGAAAGGCGGGGGGTCCAGGAGGACGCG GAGCACACCCCTCCTGAATCAGCAATTAGACACTTTCGGCCCCCAGGTCCTCCTGGGG GAGCACACCCCTCCTGAATCAGCAATTAGACACTTTCGGCCCCCAGGTCCTCCTGGGG

4514 DRD1, 4517 TTH3I,

- ProGlnProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAla 4622 CCACAACCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAAACGTGTCAGTCGCC GGTGTTGGTCTTATGCTGAACCTCAGGTATTGTAGTACGAGGAGGTTCACAGTCAGCGG

4643 SACI,

HisAspGlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAla CACGACGGCGCTGGAAAGAGGTCTTACTCACCCGTGACCCTACACCCCCTCGCG GTGCTGCCGCGACCTTTCTCCCAGATGATGGGATGTGGGATGTTGGGGATCTTG

4737 NRUI,

- ArgAlaAlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIle 4742 AGAGCTGCGTGGGAACAACACACACTCCAGTCAATTCCTGGCTAGGCAACATAATC TCTGGACGCACCCTTCTGTCTGTGTGAGTCAGTTAAGGACCGATCCGTTGTATTAG

4812 PFLM1, 4813 DRA3,

IleAlaArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSer 4862 ATAGCCAGGACCAGCTTGAACAGCCCTCGATTGCGAGATCTAGGGGCCTGCTACTCC TATGGGTCCCTGGTCGAACTTGTCCGGAGCTAACGCTCTAGATGCCCCGAGCGATGAGG

4899 BGL2,

IleGluProLeuAspLeuProProllelleGlnArgLeuHisGlyLeuSerAlaPheSer
4922 ATAGAACCACTGGATCTACCTCCAATCATTCAAAGCATCGCCTCAGGGCATTTTCA
TATCTTGGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAAGT

4960 NCOI.

LeuHisserTyrSerProGlyGluIleAsnArgValAlaAlaCysLeuArgLysLeuGly CTCCACAGTTACTCTCCAGGTGAAATCAATAGGGTGGCGCATGCCTCAGAAACTTGGG GAGGTGTCAATAGAGAGGTCCACTTTAGTTATTATCCCACCGGGTTACGGAGTCTTTTGAACCG

5021 SPHI, 5041 KPNI.

3722	TTTGACAGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGGAGGTTAAAGCAAACTGTCTGACGTTCAAGACCTGTCGGTAATGGTCCTGCATGAGTTCCTCCAATTTCG
3782	AlaalaSerLysValLysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrPrr GCGGCGTCAAAAGTGAAGGCTAACTTGCTATCCGTACAGGAAGCTTGCAGCCTGACGCC CGCCGCAGTTTTCACTTCCGATTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGC
	3822 HIND3,
3842	ProHisserAlaLysserLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArg CCACACTCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCGGTGCCATGCCAG GGTGTGAGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCT
	3881 AAT2, 3896 BGLI,
3902	LysAlaValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrPro AAGGCCGTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACACCA TTCCGGCATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGT
3962	IleAspThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGly ATAGACACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGGT TATCTGTGATGGTAGTACCGATTCTTGCTCCAAAAGACGCAAGTCGGACTCTTTCCCCCCA
4022	ArgLysProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMet CGTAAGCCAGCTCGTCTCATCGTGTTCCCGGATCTGGGCGTGCGCGTGTGCGAAAAGATG GCATTCGGTCGAGCAGAGGAGCACAGGGGCTAGACCCGCACCGCACACGCTTTTCTAC
4082	AlaLeuTyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPhe GCTTTGTACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCTCCTACGGATTC CGAAACATGCTGCACCAATGTTTCGAGGGGAACCCGCACTACCCTTCGAGGATGCCTAAG
4142	GlnTyrSerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThr CAATACTCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACC GTTATGAGTGGTCCTGTCGCCCAACTTAAGGAGCACGTTCGCACCTTCAGGTTCTTTTGG
	4166 ECORI,
4202	ProMetGlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIle CCAATGGGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATC GGTTACCCCAAGAGCATACTATGGGCGACGAAACTGAGGTGTCAGTGACTCTCGCTGTAG
	4235 DRD1, 4242 ALWN1,
1262	ArgthrGluGluAlaIletyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIle CGTACGGAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCGTGGCCATC GCATGCCTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGTTCGGCCGCACCGGTAG
	4307 BGLI, 4314 BALI,

CysGlyTyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeu
1382 TGCGGCTATCGCAGGTGCCGCGCGAGCGGCGTACTGACAACTAGCTGTGGTAACACCCTC

4351 APAI,

LysSerLeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsn
4322 AAGTCCTCACCGAGAGGCTTTATGTTGGGGCCCCTCTTACCAATTCAAGGGGGAGAAC
TTCAGGGAGTGGCTCCCCCCTCTTG
TTCAGGGAGTGGCTCCCCCCTCTTG

3149 ALWN1, 3170 EAG1 XMA3,

ASPPROPROLEUVAIGUTHRTTPLYSLYSPROASPTYRGUPROPROVAIVAIHISGLY
3182 ARCCCCCCGCTAGTGGAGACGTGGAAAAGCCCGACTACGACCACGTGTCCATGCC
TTGGGGGGGGATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGACACCAGGTACCG

3223 HGIE2, 3235 NCOI.

ValLeuThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGly
GTCCTCACTGAATCAACCCTATCTACTGCTGGCCGAGCTGGCCACCACAACCTTTGGC
CAGGAGTGACTTAGTTGGGAATCACGCTGAGCCGGTGGAGCGGTGGTCTTGGAACCG

3338 SACI, 3352 HIND3,

SerGlyCysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGly
TCTGGCTGCCCCCCGACTCCGACTCCGACTCATCCCTATTCCTCCATGCCCCCCCTGGAGGGG
AGACCGACGGGGGGCTTGAGGCTGCGACTCAGGATAAGGAGGTACGGGGGGACTTCCCC

3443 EAM11051,

GLUPTOGIAMSPPTOASDLEUSETASSGIJSETTTPSETTHTVAISETSETGIUALAASN GAGCCTTGGGATCCTGACCTTACCGACGGTCATGGTCAACGGTCAGTAGTGAGGCCACA CTCGGACCCCTAGGCCTAGGATCGCTGCCAGTACCAGTTGCCAGTCATCCGGTTG

3490 BAMHI, 3491 BSAB1, 3493 BSPE1,

AlaGluAspvalValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrPro GCGGAGGATGTCGTGTGCTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCG CGCTCCTACAGCACCACGACTACAATGAATGAGAACCTGTCCGCGTGAGCAGTGGGGC

3595 DRA3,

3606 SAC2, 3617 ALWN1, 3661 PFLM1,

HisAsnLeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThr
CACAATTTGGTGTATTCCACCACCTCACGCAGTGCTTGCCAAAGGCAGAAGAAAGTCACA
GTGTTAAACCACCATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGTCTTCTTTCAGTGT

3687 DRA3,

PheAspArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAla

	GTTCAGTAAC	ACTCTTATCA	CATACGCCGC	TGGCTCAACG	TCTTGCCCGG AGAACGGGCC
5851		GGATAATACC	GCGCCACATA CGCGGTGTAT	GCAGAACTTT	AAAAGTGCTC TTTTCACGAG
5901	ATCATTGGAA	AACGTTCTTC	GGGGCGAAAA	CTCTCAAGGA	TCTTACCGCT
	TAGTAACCTT	TTGCAAGAAG	CCCCGCTTTT	GAGAGTTCCT	AGAATGGCGA
5951		AGTTCGATGT TCAAGCTACA	AACCCACTCG TTGGGTGAGC	TGCACCCAAC ACGTGGGTTG	TGATCTTCAG ACTAGAAGTC
6001		TTTCACCAGC AAAGTGGTCG	GTTTCTGGGT CAAAGACCCA	GAGCAAAAAC CTCGTTTTTG	AGGAAGGCAA TCCTTCCGTT
6051	AATGCCGCAA	AAAAGGGAAT	AAGGGCGACA	CGGAAATGTT	GAATACTCAT
	TTACGGCGTT	TTTTCCCTTA	TTCCCGCTGT	GCCTTTACAA	CTTATGAGTA
6101	ACTCTTCCTT	TTTCAATATT	ATTGAAGCAT	TTATCAGGGT	TATTGTCTCA
	TGAGAAGGAA	AAAGTTATAA	TAACTTCGTA	AATAGTCCCA	ATAACAGAGT
6151	TGAGCGGATA	CATATTTGAA	TGTATTTAGA	AAAATAAACA	AATAGGGGTT
	ACTCGCCTAT	GTATAAACTT	ACATAAATCT	TTTTATTTGT	TTATCCCCAA
6201	CCGCGCACAT	TTCCCCGAAA	AGTGCCACCT	GACGTCTAAG	AAACCATTAT
	GGCGCGTGTA	AAGGGGCTTT	TCACGGTGGA	CTGCAGATTC	TTTGGTAATA
6251	TATCATGACA	TTAACCTATA	AAAATAGGCG	TATCACGAGG	CCCTTTCGTC
	ATAGTACTGT	AATTGGATAT	TTTTATCCGC	ATAGTGCTCC	GGGAAAGCAG

FIG. 9-Page 8

		r			
4851	AGCAGAGCGA TCGTCTCGCT	GGTATGTAGG	COCTOCTAC	A GAGTTCTTG	A AGTGGTGGCC
4901	TAACTACGG	TACACTAGAA	GGACAGTAT	f TGGTATCTG	CGCTCTGCTGA
_	ATTGATGCCC	ATGTGATCTT	CCTGTCATA	ACCATAGACO	CGAGACGACT
4951	AGCCAGTTAC	CTTCGGAAAA	AGAGTTGGT	A GCTCTTGATO	CGGCAAACAA
_	TCGGTCAATC	GAAGCCTTTT	TCTCAACCAT	CGAGAACTA	GCCGTTTGTT
5001	ACCACCGCTG	GTAGCGGTGG	TTTTTTTGTT	TGCAAGCAG	AGATTACGCG
	TGGTGGCGAC	CATCGCCACC	AAAAAAACA	ACGTTCGTCG	TCTAATGCGC
5051	CAGAAAAAA	GGATCTCAAG	AAGATCCTTT	GATCTTTCT	ACGGGGTCTG
	GTCTTTTTT	CCTAGAGTTC	TTCTAGGAAA	CTAGAAAAGA	TGCCCCAGAC
5101	ACGCTCAGTG	GAACGAAAAC	TCACGTTARG		CATGAGATTA
	TGCGAGTCAC	CTTGCTTTTG	AGTGCAATTC	CCTAAAACCA	GTACTCTAAT
5151	TCAAAAAGGA	TCTTCACCTA	CATCCTTTTA	*********	GAAGTTTTAA
	AGTTTTCCT	AGAAGTGGAT	CTAGGAAAAT	TTAATTTTTA	CTTCAAAATT
	10011000				
5201	TAGTTAGATT	AGTATATATG TCATATATAC	AGTAAACTTG	GTCTGACAGT	TACCAATGCT ATGGTTACGA
5251	TAATCAGTGA	GGCACCTATC	TCAGCGATCT	GTCTATTTCG	TTCATCCATA AAGTAGGTAT
	ATTAGTCACT	CCGTGGATAG	AGTCGCTAGA	CAGATAAAGC	AAGTAGGTAT
5301	GTTGCCTGAC	TCCCCGTCGT	GTAGATAACT	ACGATACGGG	AGGGCTTACC
	CAACGGACTG	AGGGGCAGCA	CATCTATTGA	TGCTATGCCC	TCCCGAATGG
5351	ATCTGGCCCC	AGTGCTGCAA	TGATACCGCG	AGACCCACGC	TCACCGGCTC
	TAGACCGGGG	TCACGACGTT	ACTATGGCGC	TCTGGGTGCG	AGTGGCCGAG
5401	CAGATTTATC	AGCAATAAAC	CAGCCAGCCG	GAAGGGCCGA	GCGCAGAAGT
	GTCTAAATAG	TCGTTATTTG	GTCGGTCGGC	CTTCCCGGCT	CGCGTCTTCA
5451	GGTCCTGCAA	CTTTATCCGC	CTCCATCCAG	TCTATTAATT	CTTCCCCCC
	CCAGGACGTT	GAAATAGGCG	GAGGTAGGTC	AGATAATTAA	CAACGGCCCT
501	1000000000				
,501	TCGATCTCAT	TCATCAAGCG	GTCAATTATC	TTTGCGCAAC AAACGCGTTG	CAACAACGGT
551	TTGCTACAGG	CATCGTGGTG	TCACGCTCGT	CGTTTGGTAT GCAAACCATA	GGCTTCATTC
	AACGATGTCC	GIAGCACCAC	AGTGCGAGCA	GCAAACCATA	CCGAAGTAAG
601	AGCTCCGGTT	CCCAACGATC	AAGGCGAGTT	ACATGATCCC	CCATGTTGTG
	TCGAGGCCAA	GGGTTGCTAG	TTCCGCTCAA	TGTACTAGGG	GGTACAACAC
651	CAAAAAAGCG	GTTAGCTCCT	TCGGTCCTCC	GATCGTTGTC	AGAAGTAAGT
	GTTTTTTCGC	CAATCGAGGA	AGCCAGGAGG	CTAGCAACAG	TCTTCATTCA
701	TGGCCGCAGT	GTTATCACTC	ATGGTTATGG	CAGCACTGCA	TAATTCTCTT
_	ACCGGCGTCA	CAATAGTGAG	TACCAATACC	GTCGTGACGT	ATTAAGAGAA
751	ACTGTCATGC	CATCCCTARC	3.TCCTTTTT	CRC3 CRCC	

			DCM V-NS	34A	
3951	GCGTGGTC	I V G I AT AGTGGGCAG TA TCACCCGTG	G GTCGTCTT	OT CCGGGAAGC	P A I I C GGCAATCATA G CCGTTAGTAT
4001	P D R CCTGACAGO GGACTGTCC	E V L GG AAGTCCTCT CC TTCAGGAGA	TA CCGAGAGT	F D E M TC GATGAGATG AG CTACTCTAC	E E C G AAGAGTGCTA C TTCTCACGAT
	BamHI	MluI			
4051	GGATCCACT CCTAGGTGA	A CGCGTTAGA	G CTCGCTGA	C AGCCTCGAC AG TCGGAGCTG	T GTGCCTTCTA A CACGGAAGAT
4101	GTTGCCAGC CAACGGTCG	C ATCTGTTGT G TAGACAACA	T TGCCCCTCC A ACGGGGAGC	C CCGTGCCTT	C CTTGACCCTG G GAACTGGGAC
4151	GAAGGTGCC CTTCCACGG	A CTCCCACTG T GAGGGTGAC	T CCTTTCCTA A GGAAAGGAT	A TAAAATGAG	G AAATTGCATC C TTTAACGTAG
4201	GCATTGTCT CGTAACAGA	G AGTAGGTGT C TCATCCACA	C ATTCTATTO	T GGGGGGTGG	G GTGGGGCAGG CACCCCGTCC
4251	ACAGCAAGG TGTCGTTCC	G GGAGGATTG	G GAAGACAAT C CTTCTGTTA	A GCAGGCATGO T CGTCCGTACO	TGGGGAGCTC ACCCCTCGAG
4301	TTCCGCTTCC AAGGCGAAGC	TCGCTCACT	G ACTCGCTGC C TGAGCGACG	G CTCGGTCGTT C GAGCCAGCA	CGGCTGCGGC
4351	GAGCGGTATO CTCGCCATAO	AGCTCACTCA TCGAGTGAGT	A AAGGCGGTA TTCCGCCAT	A TACGGTTATO	CACAGAATCA GTGTCTTAGT
4401	GGGGATAACC CCCCTATTGC	CAGGAAAGAA GTCCTTTCTT	CATGTGAGC GTACACTCG	A AAAGGCCAGC T TTTCCGGTCG	AAAAGGCCAG TTTTCCGGTC
1451 (	GAACCGTAAA CTTGGCATTT	AAGGCCGCGT TTCCGGCGCA	TGCTGGCGT	TTTCCATAGG A AAAGGTATCC	CTCCGCCCCC GAGGCGGGGG
1501	TGACGAGCA GACTGCTCGT	TCACAAAAAT AGTGTTTTTA	CGACGCTCA	A GTCAGAGGTG CAGTCTCCAC	GCGAAACCCG CGCTTTGGGC
551 7	CAGGACTAT GTCCTGATA	AAAGATACCA TTTCTATGGT	GGCGTTTCCC	CCTGGAAGCT GGACCTTCGA	CCCTCGTGCG GGGAGCACGC
601 G	TCTCCTGTT AGAGGACAA	CCGACCCTGC	CGCTTACCGC	ATACCTGTCC TATGGACAGG	GCCTTTCTCC CGGAAAGAGG
651 C	TTCGGGAAG AAGCCCTTC	CGTGGCGCTT GCACCGCGAA	TCTCAATGCT AGAGTTACGA	CACGCTGTAG	GTATCTCAGT CATAGAGTCA
701 T	CGGTGTAGG GCCACATCC	TCGTTCGCTC AGCAAGCGAG	CAAGCTGGGC GTTCGACCCG	TGTGTGCACG ACACACGTGC	AACCCCCCGT TTGGGGGGCA
751 T	CAGCCCGAC GTCGGGCTG	CGCTGCGCCT GCGACGCGGA	TATCCGGTAA ATAGGCCATT	CTATCGTCTT GATAGCAGAA	GAGTCCAACC CTCAGGTTGG
801 C	GGTAAGACA	CGACTTATCG	CCACTCCCAC	CAGCCACTGG GTCGGTGACC	

2486 ASE1, 2503 APAI,

ProAlaProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIle
2522 CTGGGCGAACTACACGTTGGGGCTATGGAGGTGTCTGCAGAGGAATACGTGGAGTA
GGAGGGGGTTGATGTGCAAGGGCGATACCTCCCACAGAGGTCTCCTTATGCACCTCTAT

2559 PSTI.

ArgGinValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysPro
AGGCAGGTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTTAAATGCCGG
TCCGTCCACCCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTTACGGGC

2600 DRA3.

- CysGlnValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPhe
  TGCCAGGTCCCATCGCCCGAATTTTTCACAGAATTGGACGGGTGCGCCTACATAGGTTT
  ACGGTCCAGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAA
- AlaProProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGlu GCGCCCCCCTGCAAGCCCTTGCTGCGGAAGGAGGTATCATTCAGAGTAGGACTCCACGAA CGCGGGGGGACGTTCGGGAACGACGCCCTCCTCCATAGTAAGTCTCATCCTGAGGTGCTT
- TyrProValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSer
  TACCGGTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCC
  ATGGCCATCCCAGCGTTAATGGAACGCTCGGGCTTGCACCGGCACAACTGCAGG

2763 HGIE2, 2815 AAT2,

2856 EAG1 XMA3,

SerProProSerValAlaSerSerSerAlaSerGinLeuSerAlaProSerLeuLysAla
TOACCCCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCA
AGTGGGGGAGACACCGGTCGAGGAGCCGATCGGTCGATGGGGGAGTTCGGT

2895 BALI, 2909 NHEI,

ThrCysThrAlaAsHHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrp 2942 ACTTGCACGGCTAACCATGACTCCCCTGATGCTGATGCTGATGAGAGGCAACCTCCTATGG TGAACGTGGCGATTGGTACTGAGGGGACTACGACTTACTCCCGGTTGGAGGATACC

2972 ESP1, 2975 SACI,

- AspserpheAspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGlu
  3062 GACTCCTTCGATCGCTTGTGGCGGAGGAGGAGGAGGAGGAGATCTCGGTAGCGGAGAA
  CTGAGGAAGCTAGGGGACACCGCCTCCTCTCTCTCCCCCTTAGAGGCATGGGGGTCTT

3102 BGL2,

+2 G D F D S V I D C N T C V T Q T V 3251 GGCGACTTCG ACTCGGTGAT AGACTGCAAT ACGTGTGTCA CCCAGACAGT CCGCTGAAGC TGAGCCACTA TCTGACGTTA TGCACACAGT GGGTCTGTCA +2 D F S LDPT FTI ETITLP 3301 CGATTTCAGC CTTGACCCTA CCTTCACCAT TGAGACAATC ACGCTCCCCC GCTAAAGTCG GAACTGGGAT GGAAGTGGTA ACTCTGTTAG TGCGAGGGGG +2 Q D A V S R T QRRG RTG 3351 AAGATGCTGT CTCCCGCACT CAACGTCGGG GCAGGACTGG CAGGGGGAAG TTCTACGAGA GAGGGCGTGA GTTGCAGCCC CGTCCTGACC GTCCCCCTTC +2 P G I Y RFVAPG ERPS 3401 CCAGGCATCT ACAGATTTGT GGCACCGGGG GAGCGCCCCT CCGGCATGTT GGTCCGTAGA TGTCTAAACA CCGTGGCCCC CTCGCGGGGA GGCCGTACAA +2 DSSVLCECYD AGC 3451 CGACTCGTCC GTCCTCTGTG AGTGCTATGA CGCAGGCTGT GCTTGGTATG GCTGAGCAGG CAGGAGACAC TCACGATACT GCGTCCGACA CGAACCATAC +2 E L T P A E T T V R L 3501 AGCTCACGCC CGCCGAGACT ACAGTTAGGC TACGAGCGTA CATGAACACC TCGAGTGCGG GCGGCTCTGA TGTCAATCCG ATGCTCGCAT GTACTTGTGG +2 P G L P V C Q DHLEFWE G V F 3551 CCGGGGCTTC CCGTGTGCCA GGACCATCTT GAATTTTGGG AGGGCGTCTT GGCCCCGAAG GGCACACGGT CCTGGTAGAA CTTAAAACCC TCCCGCAGAA T G L T H I D A H F L S Q T K Q +2 StuI 3601 TACAGGCCTC ACTCATATAG ATGCCCACTT TCTATCCCAG ACAAAGCAGA ATGTCCGGAG TGAGTATATC TACGGGTGAA AGATAGGGTC TGTTTCGTCT +2 S G E N LPY LVAYOAT 3651 GTGGGGAGAA CCTTCCTTAC CTGGTAGCGT ACCAAGCCAC CGTGTGCGCT CACCCCTCTT GGAAGGAATG GACCATCGCA TGGTTCGGTG GCACACGCGA +2 R A Q A PPP S W D Q M W K 3701 AGGGCTCAAG CCCCTCCCCC ATCGTGGGAC CAGATGTGGA AGTGTTTGAT TCCCGAGTTC GGGGAGGGG TAGCACCCTG GTCTACACCT TCACAAACTA RLKPTLHGPT PLL 3751 TCGCCTCAAG CCCACCCTCC ATGGGCCAAC ACCCCTGCTA TACAGACTGG AGCGGAGTTC GGGTGGGAGG TACCCGGTTG TGGGGACGAT ATGTCTGACC +2 G A V Q N E I T L T H PVTKYI 3801 GCGCTGTTCA GAATGAAATC ACCCTGACGC ACCCAGTCAC CAAATACATC CGCGACAAGT CTTACTTTAG TGGGACTGCG TGGGTCAGTG GTTTATGTAG +2 M T C M S A D LEV VTST 3851 ATGACATGCA TGTCGGCCGA CCTGGAGGTC GTCACGAGCA CCTGGGTGCT TACTGTACGT ACAGCCGGCT GGACCTCCAG CAGTGCTCGT GGACCCACGA V G G +2 V L A A L A A YCL 3901 CGTTGGCGGC GTCCTGGCTG CTTTGGCCGC GTATTGCCTG TCAACAGGCT

penty 11334A
+2 N S S P P V V P Q S F Q V A H L 2551 TAACTCCTCT CCACCAGTAG TGCCCCAGAG CTTCCAGGTG GCTCACCT ATTGAGGAGA GGTGGTCATC ACGGGGTCTC GAAGGTCCAC CGAGTGGA
+2 H A P T G S G K S T K V P A A Y .  2601 ATGCTCCCAC AGGCAGGGC AAAAGCACCA AGGTCCCGGC TGCATATGC TACGAGGGTG TCCGTCGCCG TTTTCGTGGT TCCAGGGCCG ACGTATACC
+2 A Q G Y K V L V L N P S V A A T 2651 GCTCAGGGCT ATAAGGTGCT AGTACTCAAC CCCTCTGTTG CTGCAACAC CGAGTCCCGA TATTCCACGA TCATGAGTTG GGGAGACAAC GACGTTGTC
+2 G F G A Y M S K A H G I D P N I 2701 GGGCTTTGGT GCTTACATGT CCAAGGCTCA TGGGATCGAT CCTAACATC CCCGAAACCA CGAATGTACA GGTTCCGAGT ACCCTAGCTA GGATTGTAC
+2 R T G V R T I T T G S P I T Y S T 2751 GGACCGGGGT GAGAACAATT ACCACTGGCA GCCCCATCAC GTACTCCAC CCTGGCCCCA CTCTTGTTAA TGGTGACCGT CGGGGTAGTG CATGAGGTG
+2 Y G K F L A D G G C S G G A Y D 2801 TACGCCAGT TCCTTGCCGA CGGCGGGTGC TCGGGGGGGC CTTATGACA ATGCCGTTCA AGGAACGGCT GCCGCCCACG AGCCCCCCGC GAATACTGT
+2 I I C D E C H S T D A T S I L G 2851 AATAATTTG GACGAGTGCC ACTCCACGGA TGCCACATCC ATCTTGGGC TTATTAAACA CTGCTCACGG TGAGGTGCCT ACGGTGTAGG TAGAACCCG
+2 I G T V L D Q A E T A G A R L V V 2901 TTGGCACTGT CCTTGACCAA GCAGAGACTG CGGGGGCGAG ACTGGTTGTG AACCGTGACA GGAACTGGTT CGTCTCTGAC GCCCCCGCTC TGACCAACAC
+2 L A T A T P P G S V T V P H P N 1 2951 CTCGCCACCG CCACCCCTCC GGGCTCCGTC ACTGTGCCCC ATCCCAACA: GAGCGGTGGC GGTGGGGAGG CCCGAGGCAG TGACACGGGG TAGGGTTGTF
+2 E E V A L S T T G E I P F Y G K 3001 CGAGGAGGTT GCTCTGTCCA CCACCGGAGA GATCCCTTTT TACGGCAAGG GCTCCTCCAA CGAGACAGGT GGTGGCCTCT CTAGGGAAAA ATGCCGTTCC
+2 A I P L E V I K G G R H L I F C H 3051 CTATCCCCCT CGAAGTAATC AAGGGGGGGA GACATCTCAT CTTCTGTCAT GATAGGGGGA GCTTCATTAG TTCCCCCCCT CTGTAGAGTA GAAGACAGTA
+2 S K K K C D E L A A K L V A L G I 3101 TCAAAGAAGA AGTGCGACGA ACTCGCCGCA AAGCTGGTCG CATTGGGCAT AGTTTCTTCT TCACGCTGCT TGAGCGGCGT TTCGACCAGC GTAACCCGTA
+2 N A V A Y Y R G L D V S V I P T 3151 CAATGCCGTG GCCTACTACC GCGGTCTTGA CGTGTCCGTC ATCCCGACCA GTTACGGCAC CGGATGATGG CGCCAGAACT GCACAGGCAG TAGGGCTGGT
+2 S G D V V V V A T D A L M T G Y T 3201 GCGGCGATGT TETCGTG GCAACCGATG CCCTCATGAC CGGCTATACC CGCCGCTACA ACAGCAGCAC CGTTGGCTAG GGGGATATTG GCCGTATACG

		pC	MV-NS34	A	
1851	TTAACGGTGG AGG	GCAGTGT CCGTCACA	AGTCTGAGCA TCAGACTCGT	GTACTCGTTG CATGAGCAAC	CTGCCGCGCG
1901	CGCCACCAGA CAT GCGGTGGTCT GTA	AATAGCT TTATCGA	GACAGACTAA CTGTCTGATT	CAGACTGTTC GTCTGACAAG	CTTTCCATGO GAAAGGTACO
٠	2			EcoRI	M A P
1951	GTCTTTTCTG CAG CAGAAAAGAC GTC	TCACCGT AGTGGCA	CGTCGACCTA GCAGCTGGAT	AGAATTCACC TCTTAAGTGG	ATGGCGCCCA TACCGCGGGT
2001	2 I T A Y A TCACGGCGTA CGC AGTGCCGCAT GCG	CCAGCAG	T R G I ACAAGGGGCC TGTTCCCCGG	TOOTNOOCTO	I I T CATAATCACO GTATTAGTGO
2051	S L T G AGCCTAACTG GCC TCGGATTGAC CGG	R D K GGGACAA CCCTGTT	N Q V AAACCAAGTG ITTGGTTCAC	E G E V GAGGGTGAGG CTCCCACTCC	TOCACATTOT
2101	S T A A GTCAACTGCT GCC CAGTTGACGA CGG	Q T F CAAACCT : GTTTGGA ;	L A T CCTGGCAAC AGGACCGTTG	C I N GTGCATCAAT CACGTAGTTA	G V C GGGGTGTGCT CCCCACACGA
2151	W T V Y H GGACTGTCTA CCA CCTGACAGAT GGT	G A CGGGGCC C	G T R T GGAACGAGGA CCTTGCTCCT	CCATCGCGTC	P K G ACCCAAGGGT TGGGTTCCCA
2201	P V I Q P CCTGTCATCC AGA: GGACAGTAGG TCT	GTATAC C	N V D CAATGTAGAC CTTACATCTG	Q D L V CAAGACCTTG GTTCTGGAAC	TECCCTCCCC
2251	A S Q G CGCTTCGCAA GGTA GCGAAGCGTT CCAT	T R S	L T P ATTGACACC ( TAACTGTGG (	C T C CTGCACTTGC ( GACGTGAACG (	G S S GGCTCCTCGG CCGAGGAGCC
2301	D L Y L V ACCTTTACCT GGTC TGGAAATGGA CCAG	ACGAGG C	H A D V ACGCCGATG 1 TGCGGCTAC A	CATTCCCGT (	R R R GCGCCGGCGG GCGGCCGCC
2351	G D S R G GGTGATAGCA GGGG CCACTATCGT CCCC	CAGCCT G	L S P CTGTCGCCC C GACAGCGGG C	R P I S GGCCCATTT ( GCCGGGTAAA (	Y L K CCTACTTGAA GGATGAACTT
2401	G S S G AGGCTCCTCG GGGG TCCGAGGAGC CCCC	G P L GTCCGC T CAGGCG A	L C P GTTGTGCCC C CAACACGGG G	A G H GCGGGGGCAC G GCGCCCCGTG C	A V G GCCGTGGGCA
2451	I F R A A TATTTAGGGC CGCG ATAAATCCCG GCGC	GTGTGC A	T R G V CCCGTGGAG T GGGCACCTC A	A K A GGCTAAGGC G CCGATTCCG C	V D F GTGGACTTT CACCTGAAA
2501	I P V E N ATCCCTGTGG AGAA TAGGGACACC TCTT	L E CCTAGA GA GGATCT C	ACAACCATG A	R S P V GGTCCCCGG T CCAGGGGCC A	F T D GTTCACGGA CAAGTGCCT

901	TTTTGGCAC AAAACCGTG	C AAAATCAAC G TTTTAGTTG	G GGACTTTCC	A AAATGTCGT T TTTACAGCA	A ATAACCCCGC T TATTGGGGCG
951		G CAAATGGGC C GTTTACCCG	G GTAGGCGTG	T ACGGTGGGA A TGCCACCCT	G GTCTATATAA C CAGATATATT
1001		G TTTAGTGAA C AAATCACTT	C CGTCAGATCO G GCAGTCTAGO	GGACCTCTG	G CCATCCACGC GGTAGGTGCG
1051	TGTTTTGAC ACAAAACTG	C TCCATAGAA G AGGTATCTT	G ACACCGGGAC C TGTGGCCCTC	CGATCCAGC	TCCGCGGCCG AGGCGCCGGC
1101	GGAACGGTGG CCTTGCCACG	C ATTGGAACG C TAACCTTGC	G GGATTCCCCC	TGCCAAGAG:	GACGTAAGTA CTGCATTCAT
1151	CCGCCTATA GGCGGATAT	G ACTCTATAGE C TGAGATATC	G CACACCCCTT	TGGCTCTTAT	GCATGCTATA CGTACGATAT
1201	CTGTTTTTGC GACAAAAACC	GAACCCCGG	ATACACCCCC	GCTCCTTATO	CTATAGGTGA CGATATCCACT
1251	TGGTATAGCT ACCATATCG	TAGCCTATAC ATCGGATATO	GTGTGGGTTA CACACCCAAT	TTGACCATTA AACTGGTAAT	TTGACCACTC
1301	CCCTATTGGT GGGATAACCA	GACGATACT	TCCATTACTA AGGTAATGAT	ATCCATAACA TAGGTATTGT	TGGCTCTTTG ACCGAGAAAC
1351	CCACAACTAT GGTGTTGATA	CTCTATTGGC	TATATGCCAA ATATACGGTT	TACTCTGTCC	TTCAGAGACT AAGTCTCTGA
1401	GACACGGACT CTGTGCCTGA	CTGTATTTT GACATAAAA	ACAGGATGGG TGTCCTACCC	GTCCATTTAT CAGGTAAATA	TATTTACAAA ATAAATGTTT
1451	TTCACATATA AAGTGTATAT	CAACAACGCC GTTGTTGCGG	GTCCCCCGTG CAGGGGGCAC	CCCGCAGTTT GGGCGTCAAA	TTATTAAACA AATAATTTGT
1501	TAGCGTGGGA ATCGCACCCT	TCTCCGACAT AGAGGCTGTA	CTCGGGTACG GAGCCCATGC	TGTTCCGGAC ACAAGGCCTG	ATGGGCTCTT TACCCGAGAA
1551	CTCCGGTAGC GAGGCCATCG	GGCGGAGCTT CCGCCTCGAA	CCACATCCGA GGTGTAGGCT	GCCCTGGTCC CGGGACCAGG	CATCCGTCCA GTAGGCAGGT
1601	GCGGCTCATG CGCCGAGTAC	GTCGCTCGGC CAGCGAGCCG	AGCTCCTTGC TCGAGGAACG	TCCTAACAGT AGGATTGTCA	GGAGGCCAGA CCTCCGGTCT
1651	CTTAGGCACA GAATCCGTGT	GCACAATGCC CGTGTTACGG	CACCACCACC GTGGTGGTGG	AGTGTGCCGC TCACACGGCG	ACAAGGCCGT TGTTCCGGCA
1701	GGCGGTAGGG CCGCCATCCC	TATGTGTCTG ATACACAGAC	AAAATGAGCT TTTTACTCGA	CGGAGATTGG GCCTCTAACC	GCTCGCACCT CGAGCGTGGA
1751	GGACGCAGAT CCTGCGTCTA	GGAAGACTTA CCTTCTGAAT	AGGCAGCGGC TCCGTCGCCG	AGAAGAAGAT TCTTCTTCTA	GCAGGCAGCT CGTCCGTCGA
1801	GAGTTGTTGT CTCAACAACA	ATTCTGATAA TAAGACTATT	GAGTCAGAGG CTCAGTCTCC	TAACTCCCGT ATTGAGGGCA	TGCGGTGCTG ACGCCACGAC

	1 TCGCGCGTT AGCGCGCAA	TT CGGTGATGA NA GCCACTACT	C GGTGAAAAC	C TCTGACACA	GCAGCTCCCG CGTCGAGGGC
51	GAGACGGTC CTCTGCCAG	A CAGCTTGTC	T GTAAGCGGA A CATTCGCCT	T GCCGGGAGC	A GACAAGCCCG CTGTTCGGGC
101		G TCAGCGGGT	G TTGGCGGGT	G TCGGGGCTGG	GAATTGATAC
151	CGGCATCAG GCCGTAGTG	A GCAGATTGT T CGTCTAACA	A CTGAGAGTG T GACTCTCAC	C ACCATATGA G TGGTATACT	GCTTTTTGCA CGAAAAACGT
		tuI			
201	AAAGCCTAG	G CCTCCAAAA C GGAGGTTTT	A AGCCTCCTC T TCGGAGGAG	A CTACTTCTGG	AATAGCTCAG TTATCGAGTC
251	AGGCCGAGG TCCGGCTCC	C GGCCTCGGCG G CCGGAGCCGG	C TCTGCATAA G AGACGTATT	A TAAAAAAAA T ATTTTTTA	TAGTCAGCCA
301	TGGGGCGGA ACCCCGCCT	G AATGGGCGG/C TTACCCGCCT	A ACTGGGCGGG	G GAGGGAATTA C CTCCCTTAAT	TTGGCTATTG AACCGATAAC
351	GCCATTGCA CGGTAACGT	F ACGTTGTATO	TATATCATA	TATGTACATT	TATATTGGCT ATATAACCGA
401	CATGTCCAA: GTACAGGTT	TATGACCGCCA TACTGGCGGT	TGTTGACATT	GATTATTGAC CTAATAACTG	TAGTTATTAA ATCAATAATT
451	TAGTAATCA! ATCATTAGT	A TTACGGGGTC	ATTAGTTCAT TAATCAAGTA	AGCCCATATA TCGGGTATAT	TGGAGTTCCG ACCTCAAGGC
501	CGTTACATA GCAATGTAT	CTTACGGTAA GAATGCCATT	ATGGCCCGCC TACCGGGCGC	TGGCTGACCG	CCCAACGACC GGGTTGCTGG
551	CCCGCCCATT GGGCGGGTAA	GACGTCAATA CTGCAGTTAT	ATGACGTATG	TTCCCATAGT AAGGGTATCA	AACGCCAATA TTGCGGTTAT
601	GGGACTTTCC CCCTGAAAGG	ATTGACGTCA TAACTGCAGT	ATGGGTGGAG TACCCACCTC	TATTTACGGT ATAAATGCCA	AAACTGCCCA TTTGACGGGT
651	CTTGGCAGTA GAACCGTCAT	CATCAAGTGT GTAGTTCACA	ATCATATGCC TAGTATACGG	AAGTCCGCCC TTCAGGCGGG	CCTATTGACG GGATAACTGC
701	TCAATGACGG AGTTACTGCC	TAAATGGCCC ATTTACCGGG	GCCTGGCATT CGGACCGTAA	ATGCCCAGTA TACGGGTCAT	CATGACCTTA GTACTGGAAT
751	CGGGACTTTC GCCCTGAAAG	CTACTTGGCA GATGAACCGT	GTACATCTAC CATGTAGATG	GTATTAGTCA CATAATCAGT	TCGCTATTAC AGCGATAATG
901	CATGGTGATG GTACCACTAC	CGGTTTTGGC GCCAAAACCG	AGTACACCAA TCATGTGGTT	TGGGCGTGGA ACCCGCACCT	TAGCGGTTTG ATCGCCAAAC
851	ACTCACGGGG TGAGTGCCCC	ATTTCCAAGT TAAAGGTTCA	CTCCACCCCA GAGGTGGGGT	TTGACGTCAA AACTGCAGTT	TGGGAGTTTG ACCCTCAAAC

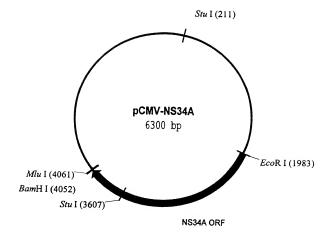


FIG. 8

#### DCMV-II

				C.	pCMV-II			
3521	TTGCCATTGC	TIGCCATICC TACAGGCATC GIGGTGTCAC GCTCGTCGTT IGGTAIGGGT ICATICAGCT AAGGGTAACG ATGTCGGTAG CACCACAGTG CGAGCAGGAA ACCATACCGA AGTAAGTCGA	GTGGTGTCAC	GCTCGTCGTT	GCTCGTCGTT TGGTATGGCT CGAGCAGCAA ACCATACCGA	TCATTCAGCT AGTAAGTCGA	CCGGTTCCCA	CCGGTTCCCA ACGATCAAGG GGCCAAGGGT TGCTAGTTCC
3601	CGAGTTACAT GCTCAATGTA	CGAGTTACAT GATCCCCCAT GCTCAATGTA CTAGGGGGTA	GTTGTGCAAA		GCTCCTTCGG	AAAGCGGTTA GCTCCTTCGG TCCTCCGATC GTTGTCAGAA TTTCGCCAAT CGAGGAAGCC AGGAGGCTAG CAACAGTCTT	GTTGTCAGAA	GTAAGTTGGC
3681	CGCAGTGTTA GCGTCACAAT	TCACTCATGG AGTGAGTACC	TTATGGCAGC AATACCGTCG	TCACICATGG TTATRGGAGG ACTGCATAAT TCTCTTACTG TCATGCCATC CGTAAGATGC TTTTCTGTGA AGTGAGTACC AATACGTCG TGACGTATTA AGAGAATGAG AGTACGGTAG GCATTCTAGG AAAAGACACT	TCTCTTACTG	TCATGCCATC	TCATGCCATC CGTAAGATGC TTTTCTGTGA AGTACGGTAG GCATTCTACG AAAAGACACT	TTTTCTGTGA
3761	CTGGTGAGTA	CTCAACCAAG	TCATTCTGAG AGTAAGACTC	CTCAACCAAG TGATTCTGAG AATAGTGTAT GCGGCGACCG AGTTGCTCTT GCCGGGCGTC GAGTTGGTTC AGTAAGACTC TYATGAGATA CGCGGTGGC TCAAGGAGAA GGGGCGCAG	GCGGCGACCG	AGTTGCTCTT TCAACGAGAA	GCCCGGCGTC	AATACGGGAT TTATGCCCTA
3841	AATACCGCGC TTATGGCGCG	CACATAGCAG GTGTATCGTC	AACTTTAAAA TTGAAATTTT	AACTITAAAA GIGCICAICA TIGGAAAACG IIGAAAITII CACGAGIAGI AACCITITGC	TTGGAAAACG TTCTTCGGGG AACCTTTTGC AAGAAGCCCC	TTCTTCGGGG CGAAAACTCT CAAGGATCTT AAGAAGCCC GCTTTTGAGA GTTCCTAGAA	CGAAAACTCT GCTTTTGAGA	CAAGGATCTT
3921	ACCGCTGTTG TGGCGACAAC	ACCECTETTE AGATECAGTT CGATGTAGE CACTEGTECA CECAACTGAT TGGCGACAAC TETAGGTEAA GETACATIGG GTGAGGACGT GGGTTGATA	CGATGTAACC	CGATGTAACC CACTCGTGCA GCTACATTGG GTGAGCACGT	CCCAACTGAT	CCCAACIGAT CTICAGCAIC ITITACTITC ACCAGGGTIT GGGIIGACIA GAAGICGIAG AAAAIGAAAG IGGICGCAAA		ACCAGCGTTT
4001	CTGGGTGAGC GACCCACTCG	CIGGGIGAGC AAAAACAGGA AGGCAAAATG CGGCAAAAAA GGGAATAAGG GCGACAGGGA AAIGTTGAAT ACTCATACTC GACCCACTCG TITTIGTGCT TCGGTTTTAG GGGGTTTTTT CCCTTATTCC GGCTGTGCCT TTACAACTTA TGAGTATGAG	AGGCAAAATG TCCGTTTTAC	CCGCAAAAA GCCGTTTTTT	GGGAATAAGG	GCGACACGGA	AATGTTGAAT .	ACTCATACTC
4081	TTCCTTTTTC	AATATTATTG TTATAATAAC	AAGCATTTAT TTCGTAAATA	CAGGGTTATT GTCCCAATAA	GTCTCATGAG CGGATACATA CAGAGTACTC GCCTATGTAT	CGGATACATA 3		TTTAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
4161	TAAACAAATA ATTTGTTTAT	GGGGTTCCGC	GCACATTTCC CGTGTAAAGG	GEGGITCEGC GCACATITCC CCGAAAAGIG CCACCIGACG TCTAAGAAAC CATTATTATC AIGACATTAA CCCCAAGGCG CGTGTAAAGG GGCITTTCAC GGTGGACIGC AGAITCTITG GTAATAATAG TACTGTAATT	CCACCTGACG	CCACCTGACG TCTAAGAAAC CATTATTATC ATGACATTAA GGTGGACTGC AGATTCTTTG GTAATAATAG TACTGTAATT	CATTATTATC A	MGACATTAA
4241	CCTATAAAAA GGATATTTTT	CCTATAAAAA TAGGCGTATC ACGAGGCCCT GGATATTTT ATCCGCATAG TGCTCCGGGA	ACGAGGCCCT	TTCGTC				

#### pCMV-II

2801	i	CACTGGTAAC	AGGATTAGCA	pC GAGCGAGGTA CTCGCTCCAT	PCMV-II 1860AGGAGC CACIGGIAAC AGGAITAGGA GAGCGAGGIA IGTAGGGGGI GCIACAGGI ICITGAAGIG GIGGCCIAAC ACGETGGIGG GIGACGATIG ICCTAAIGGI CIGGCICCAI ACAICGGGG GGAIGICICA AGAACITGAC ACGGGATIG	GCTACAGAGT CGATGTCTCA	TCTTGAAGTG AGAACTTCAC	GTGGCCTAAC CACCGGATTG
2881	TACGGCTACA ATGCCGATGT	CTAGAAGGAC GATCTTCCTG	AGTATTTGGT TCATAAACCA	ATCTGCGCTC TAGACGCGAG	TACGGUTACA CTACAAGGAC AGTATITGGI AICIGGGGIC IGCIGAAGGC AGTIACCIIC GGAAAAAGAC IIGGIAGCIC AIGCGGAIGI GAICIICCIG ICAIAAACCA IAGAGGGGAG ACGACIICGG ICAAIGGAAG CCIITIICIC AACCAICGAG	AGTTACCTTC TCAATGGAAG	GGAAAAAGAG	TTGGTAGCTC AACCATCGAG
2961	TTGATCCGCC	AAACAAACCA TTTGTTTGGT	CCGCTGGTAG	CGGTGGTTTT	TIGATCCGGC AAACAAACA CCGCTGCTAG CGGTGGTTTT TYTGTTTGCA AGGAGGAGAT TAGGGGGAGA AAAAAAGGAT AACTAGGCGG TYTGTYTGGI GGGGACCAIC GCGACCAAAA AAAGAAAGGT TGGTGGTGTA ATGGGGGTGT TYTYTYCCTA	AGCAGCAGAT TCGTCGTCTA	TACGCGCAGA	AAAAAAGGAT TTTTTCCTA
3041	CTCAAGAAGA GAGTTCTTCT	TCCTTTGATC AGGAACTAG	TTTTCTACGG AAAAGATGCC	GGTCTGACGC	CICAAGAAGA ICCTITGAIC ITITCTACGG GGICTGACGC ICAGIGGAAC GAAAACICAC GILAAGGGAI ITIGGICAIG GAGIICITGI AGGAAACIAG AAAAGAIGGC CCAGACIGGG AGICACCIIG CITITGAGIG CAAIICCCIA AAACAGIAC	GAAAACTCAC	GTTAAGGGAT	TTTGGTCATG
3121	AGATTATCAA TCTAATAGTT	AAAGGATCTT TTTCCTAGAA	CACCTAGATC	CTTTTAAATT GAAAATTTAA	AGAITATGAA AAAGGAICIT CACCTAGAIC CITITAAAIT AAAAAIGAAG ITITAAATGA AICIAAAGTA IATAIGAGIA ICIAATAGII ITICCIAGAA GIGGAICIAG GAAAAITIAA ITITIACITC AAAAITIAGI TAGAITICAI AIAIACIGAI	TTTTAAATCA AAAATTTAGT	ATCTAAAGTA TAGATTTCAT	TATATGAGTA
3201	AACTTGGTCT TTGAACCAGA	GACAGTTACC CTGTCAATGG	GACAGTTACC AATGCTTAAT CTGTCAATGG TTACGAATTA	CAGTGAGGCA GTCACTCCGT	CCTATCTCAG	CGATCTGTCT	CGATCTGTCT ATTTCGTTCA TCCATAGTTG GCTAGACAGA TAAAGCAAGT AGGTATCAAC	TCCATAGTTG AGGTATCAAC
3281	CCTGACTCCC	CCTGACTCCC CGTCGTGTAG GGACTGAGGG GCAGCACATC	ATAACTACGA TATTGATGCT	TACGGGAGGG	CCTGACTCCC CETCETETA ATAACTACGA TACGGGAGGG CTTACCATCT GGCCCCAGTG CTGCAATGAT ACCGCGAGGG GGACTGAGGG GCAGCACATC TATTGATGGT ATGCCTCCC GAATGGTAGA CGGGGGTCAC GACGTTACTA TGGCGCTCTC	GGCCCCAGTG	CTGCAATGAT	ACCGCGAGAC TGGCGCTCTG
3361	CCACGCTCAC GGTGCGAGTG	CGCCTCCAGA	TTTATCAGCA	ATAAACCAGC TATTTGGTCG	CCACGCTCAC CRECTCCACA ITTATCAGGA ATAAACCAGC CAGCCGGAAG GGCCGAGGGG AGAAGTGGTG CTGGAAGTTT GGTGGGAGTG GCCGAGGTCT AAATAGTCGT TATTTGGTGG GTGGGCTTC CGGGTGGGG TCTTCACCAG GACGTTGAAA	GGCCGAGCGC 1	AGAAGTGGTC (	STGCAACTIT
3441	ATCCGCCTCC TAGGCGGAGG	ATCCAGTCTA TAGGTCAGAT	TTAATTGTTG CCGCGAAGCT AGAGTAAGTA AATTAACAAC GGCCCTTCGA TCTCATTCAT	CCGGGGAAGCT	ATCCECCTCC ATCCACTCTA TTAATTGTTG CCGGGAGGT AGAGTAAGTA GTTCGCCAGT TAATAGTTTG CGCAACGTTG TAGGGGGGG TAGGTCAGAT AATTAACAAC GGCCCTTGGA TCTCATTCAT CAAGGGGTCA ATTATCAAAC GCGTTGCAAC	GTTCGCCAGT 1	TAATAGTTTG (	CGCAACGTTG

FIG. 7-Page 5

#### pCMV-II

2081	CCAGCCATCT GGTCGGTAGA		CCTCCCCCGT	PUMV-II GITGITIGCC CCICCCCCGI GCCITCCTIG ACCTGGAG CAACAACGG GGAGGGGCA CGCAAGGAAC IGGGACCTIC	pCMV-II ACCCTGGAAG TGGGACCTTC		GTGCCACTCC CACTGTCCTT TCCTAATAAA CACGGTCAGG GTGACAGGAA AGGATTATTT	TCCTAATAAA AGGATTATTT
2161	ATGAGGAAAT TACTCCTTTA		TGTCTGAGTA	TOCATCGOAT TOTCTGAGTA GOTCTCATTC TATTCTGGGG GCTGGGGTGG GGCAGGACAC CAAGGGGGAG ACGTAGGGTA ACAGACTCAT CCACAGTAAG ATAAGACCCC CCACCCCACC	TATTCTGGGG	GGIGTGAITC TATTCIGGG GGIGGGGIGG GGCAGGACAG CCACAGTAAG ATAAGACCC CCACCCACC CCTCCTGTC	GGCAGGACAG	CAAGGGGGAG
2241	GATTGGGAAG CTAACCCTTC	ACAATAGCAG TGTTATCGTC	GCATGCTGGG	ACAATAGGAG GCATGCTGGG GAGCTCTTCC GCTTCCTCGG TCACTGACTC GCTGCGCTCG GTCGTTCGGC TGTTATGGTC GGTAGGACCC CTGGAGAGG GGAGGGGCG AGTGACTGAG CGAGGGGGG CAGGAAGCCG	GCTTCCTCGC	TCACTGACTC	GCTGCGCTCG	GTCGTTCGGC
2321	TGCGGCGAGC	TGCGGCGAGG GGTATCAGCT CACTCAAAGG CGGTAATACG GTTATCCACA GAATCAGGGG ATAACGCAGG AAAGAACATG ACGCCGCTGG CCATAGTCGA GTGAGTTTCG GCCATTATGC CAATAGGTGT CTTAGTCGCC TATTGCGTCC TTTCTTGTAC	CACTCAAAGG GTGAGTTTCC	CGGTAATACG GCCATTATGC	GTTATCCACA	GAATCAGGG ATAACGCAGG CTTAGTCCCC TATTGCGTCC	ATAACGCAGG TATTGCGTCC	AAAGAACATG
2401	TGAGCAAAAG ACTCGTTTTC	TGAGGAAAAG GCCAGCAAAA GGCCAGGAAC CGTAAAAAGG CCGCGTTGCT GGCGTTTTTC CATAGGCTCC GCCCCCTGA ACTCGTTTC CGGTCGTTT CCGGTCCTTG GCATTTTTC GGCGCAAGGA CGGCAAAAAG GTATCCGAGG GGGGGGACT	GGCCAGGAAC	GGCCAGGAAC CGTAAAAAGG CCGCGTTGCT CCGGTCCTTG GCATTTTTCC GGCGCAACGA	CCGCGTTGCT	GGCGTTTTTC	CATAGGCTCC GTATCCGAGG	GCCCCCTGA
2481	CGAGCATCAC GCTCGTAGTG	CGAGCATCAC AAAAATGGAC GCTCAAGTCA GAGGTGGGGA AACCCGACAG GACTATAAAG ATACCAGGGG TTTCCCGCTG GCTCGTAGTG TTTTTAGCTG CGAGTTCAGT CTCCACCGCT TTGGGCTGTC CTGATATTTC TATGGTCCGG AAAGGGGAAC	GCTCAAGTCA	GAGGTGGCGA	AACCCGACAG TTGGGCTGTC	GACTATAAAG CTGATATTTC	ATACCAGGCG TTTCCCCGCTG TATGGTCCGC AAAGGGGGAC	TTTCCCCCTG
2561	GAAGCTCCCT CTTCGAGGGA	CGTGCGCTCT	CCTGTTCCGA	CCTGCCGCT TACGGATAC CTGTCCGCCT TTCTCCCTTC GGGACGCCGA ATGGCCTATG GACAGCCGA AAGAGGGAAG	TACCGGATAC	CTGTCCGCCT	TTCTCCCTTC	GGGAAGCGTG
2641	GCGCTTTCTC	GCGCTITCIC AAIGCICACC CIGIAGGIAI CICACTICGG IGTAGGICGI ICGCICCAAG CIGGGCIGIG IGCACGAACC GGCGAAAGAG TIACGAGIGG GACAICCAIA GAGICAAGCC ACAICCAGA AGGAGGIIC GACCCGACAC ACGIGGIIGG	CTGTAGGTAT	CTGTAGGTAT CTCACTTCGG TGTAGGTCGT TCGCTCCAAG CTGGGCTGTG TGCACGAACC GACATCCATA GACTCAAGGC ACATCCAGGA GGCGAGGTTC GACCGACAC ACGTGCTTGG	TGTAGGTCGT	TCGCTCCAAG	CTGGGCTGTG G	TGCACGAACC ACGTGCTTGG
2721	CCCCGTTCAG GGGGCAAGTC	CCCGACCGCT	GCGCCTTATC	GGGCCTIAIC CGGTAACTAI CGTCITGAGI CCAACCGGGI AAGACAGGA TIATGGGGG GGGGGAATAG GCGATGATA GGAGAACTCA GGTGGGGCA TICTGTGGTG AATAGGGGG	CGTCTTGAGT	CCAACCCGGT A	AAGACACGAC	TATCGCCAC

FIG. 7-Page 4

#### TI-/W/Ju

1441	1	TATTTACAAA TTCACATATA ATAAATGTTT AAGTGTATAT		p GTCCCCCGTG CAGGGGGCAC	pCMV-II CAACAAGGC GTCCCCCGG CCCGAGTTT TTATTAAACA TAGGGTGGA TCTCCGAGAT GTTGTTGCGG CAGGGGGCA GGGCGTGAAA AATAATTTGT ATGGGAGCCT AGAGGTGTA	TTATTAAACA AATAATTTGT	TAGCGTGGGA ATCGCACCCT	TCTCCGACAT AGAGGCTGTA
1521	CTCGGGTACG	TGTTCCGGAC ACAAGGCCTG	CTCGGCTACG TGTTCCGGAC ATGGCCTCTT CTCCGGTAGC GGCGGAGCTT CCACATCCGA GCCCTGGTCC CATCCGTCGA GAGCCCATGC ACAAGGCCTG TACCCGAGAA GAGGCCATGG CGCCTGGAA GGTGTAGGCT GGGAGCAGG GTAGGGGG	CTCCGGTAGC	GGCGGAGCTT	CCACATCCGA GGTGTAGGCT	GCCCTGGTCC	CATCCGTCCA
1601	GCGCCTCATG	GTCGCTCGGC	GCGCCTCATG CTCGCTCGGC AGCTCCTTGC TCCTAACACT GAAGGCAGA CTTAGGGACA GCACAATGCC CACCACCACC GCCCGAGTAC CAGGGACGC TCGAGGACG AGGATTGTCA CCTCGGGTCT GAATCCGTGT CGTGTTAGGG GTGGTGGTG	TCCTAACAGT AGGATTGTCA	GGAGGCCAGA	CTTAGGCACA	GCACAATGCC	CACCACCACC
1681	AGTGTGCCGC TCACACGCCG	ACAAGGCCGT TGTTCCGGCA	AGYGTGCGGG ACAAGGCGGT GGGGTAGGG IATCTGTCTG AAAATGAGT CGGAGAITGG GGTGGCACCT GGAGGGAGAT TAGAAGGGG TGTTGGGGG CGGCATCGC AIACACAGAC TTTTACTGGA GCGTGTAACC GGAGGTGGA CCTGGGTGTA	TATGTGTCTG	AAAATGAGCT TTTTACTCGA	CGGAGATTGG	GCTCGCACCT	GGACGCAGAT
1921	GGAAGACTTA CCTTCTGAAT	AGGCAGCGC TCCGTCGCCG	GGAAGACTTA AGGCAGGGG AGAAGAGAI GCAGGCAGCT GACTTGTTGT ATTCTGATAA GAGTCAAGGG TAACTCCGGT CCTTCTGAAT TCCGTGGCG TCTTCTTCTA GGTGCGTGGA CAAGAAGA TAAGAGTATT GTGAGTGTGTC ATTGAGGGGA	GCAGGCAGCT	GAGTTGTTGT CTCAACAACA	ATTCTGATAA TAAGACTATT	GAGTCAAGGG TAACTCCCGT CTCAGTCTCC ATTGAGGGCA	TAACTCCCGT
1841	TGCGGTGCTG ACGCCACGAC	TTAACGGTGG AATTGCCACC	TOCGCTGCTG TTAACGGTGG AGGGGAGTGT AGTCTGAGGA GTACTCGTTG CTGCCGGGG GGCGCGAGA CATAATAGGT AGGCGAGGAC AATTGCCAGC TCCGCTCACA TGAGACTGGT CATGAGGAAC GAGGGGGGG GGGTGGTCT GTATTATCGA	AGTCTGAGCA TCAGACTCGT	GTACTCGTTG	CTGCCGCGC CGCCACCAGA CATAATAGCT GACGCGCGC GCGTGCTCT GTATTATCGA	CGCCACCAGA	CATAATAGCT
1921	GACAGACTAA CTGTCTGATT	CAGACTGTTC GTCTGACAAG	ECORI GACAGACTAA CACACTETTO CTITICANGE STCTITICTS CAGICACCST CSICGACCIA AGAATTCACA CTSICTGAT STCTCACAAG GAAAGGIACS CAGAAAAGAS STCAGTGGGA GCAGCTGGAT ICTIAAGICT	GTCTTTTCTG	CAGTCACCGT CGTCGACCTA GTCAGTGGCA CCAGCTGGAT	CGTCGACCTA ,		CTCGAGCAAG
	XbaI		BamHI	I MluI				
2001	TCTAGAAAGG AGATCTTTCC	CGCGCCAAGA	TOTAGAAAGG CCCCCAACA TATCAAGAT CCACTACCCG TTAGAGCTCG CTGATCACCC TCGACTGTGC CTTCTAGTTG AGATOTITCC CCCCCCTTCT ATACTTCCTA GGTGATCCCC AATCTCGAGC GACTAGTCGG AGCTGACAG GAGATCAAC	CCACTACGCG GGTGATGCGC	TTAGAGCTCG	CTGATCAGCC 1	TCGACTGTGC C	STTCTAGTTG

#### pCMV-II

721	GCCTGGCATT CGGACCGTAA	ATGCCCAGTA TACGGGTCAT	CATGACCTTA CGGGACTTTC GTACTGGAAT GCCCTGAAAG	CGGGACTITC	GCCTGGGAIT ATGCCAGTA CATGACCTTA CGGGACTTIC CTACTTGGCA GTACATCTAC GTATTAGTCA TGGCTATTAG GGGACGGTAA TAGGGGTGAT GTACTGGAAT GCCTGAAAG GATGAAGGGT CATGTAGATG GATAATGAGT AGGGATAATG	GTACATCTAC CATGTAGATG	GTATTAGTCA CATAATCAGT	TCGCTATTAC AGCGATAATG
801	CATGGTGATG	CGGTTTTGGC GCCAAAACCG	AGTACACCAA TCATGTGGTT	TGGGCGTGGA	CATGGTGATG CGGTTTTGGC AGTACACCAA TGGCGCTTGA TACCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA GTACCACTAC GCCAAAACG TCATGTGGTT ACCGGCACGT ATCGCCAAAC TGAGTGCCCC TAAAGGTTCA GAGGTGGGGG	ACTCACGGGG TGAGTGCCCC	ATTTCCAAGT TAAAGGTTCA	CTCCACCCCA
881	TTGACGTCAA AACTGCAGTT	TGGGAGTTTG ACCCTCAAAC	TGGGACTIG TTTTGGCACC AAAATCAACG ACCCTCAAAC AAAACGGTGG TTTTAGTTGC	AAAATCAACG TTTTAGTTGC	GGACTTTCCA	AAATGTCGTA TTTACAGCAT	ATAACCCCGC CCCGTTGACG TATTGGGGCG GGGCAACTGC	CCCGTTGACG
961	CAAATGGGCG GTTTACCCGC	GTAGGCGTGT CATCCGCACA	ACGGTGGGAG TGCCACCCTC	GTCTATATAA	CAAATGGGCG GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCG TTTAGTGAAC CGTCAGATCG CCTGGAGACG GTTTACCGC CATCGGCACA TGCCACCCTC CAGATATATT CGTCGAGC AAATGACTTG GCAGTCTAGG GGACCTGTG	TTTAGTGAAC AAATCACTTG	CGTCAGATCG	CCTGGAGACG
1041	CCATCCACGC	TGTTTTGACC ACAAAACTGG	CCATCCACGC TGTTTTGACC TCCATAGAAG ACACCGGGAC GGTAGGTGCG ACAAACTGG AGGTATCTTC TGTGGCCCTG	ACACCGGGAC TGTGGCCCTG	CCATCCACGC TOTITIBACC TCCATAGAAG ACACCGGGAC CGATCCAGCC TCCGCGGCG GGAAGGGTGG ATTGGAAGG GGTAGGTGGG ACAAAACTGG AGGTATCTTC TGTGGCCCTG GCTAGGTCGG AGGCGCGGC CCTTGCCACG TAACCTTGCG	TCCGCGGCCG	GGAACGGTGC	ATTGGAACGC TAACCTTGCG
1121	GGATTCCCCG CCTAAGGGGC	TGCCAAGAGT ACGGTTCTCA	GGATTCCCCG TGCCAAGAT GACGTAAGTA CCTAAGGGGC ACGCTTCTCA CTGCATTCAT	CCCCTATAG	GGAITCCCCG TCCCAAGAGT GACGTAAGTA CCGCCTATAG ACTCTATAGG CACACCCCTT TCGCTCTTAT GCATGCTATA CCTAAGGGG ACGGITCTCA TGCGAITCAT GGCGGAIATC TGAGATATCC GTGTGGGGAA ACCGAGAATA CGTACGATAT	ACTUTATAGG CACACCCOTT IGGCICTTAI GCAIGCIATA IGAGAIAICC GIGIGGGGAA ACCGAGAAIA CGIACGAIAI	TGGCTCTTAT	GCATGCTATA
1201	CTGTTTTGG GACAAAAACC	CTTGGGGCCT	CTIGGGGCCT AIACACCCCC GCICCTIAIG GAACCCCGGA IAIGIGGGGG CGAGGAAIAC	GCTCCTTATG	CIGITITIGG CITGGGGCCI AIACACCCCC GCICCIIAIG CIAIAGGIGA IGGIAIAGCI TAGCCIAIAG CIGIGGCITA GACAAAACC GAACCCCGGA IAIGIGGGGG CGAGGAAIAC GAIAICCACI ACCAIAIGGA AICGGAIAIC CACACCAAI	CTATAGGTGA TGGTATAGCT TAGCCTATAG GATATCCACT ACCATATCGA ATGGGATATC	TAGCCTATAG	GTGTGGGTTA
1281	TTGACCATTA	TTGACCACTC AACTGGTGAG	TTGACCACTC CCCTATTGGT GACGATACTT TCCATTACTA AACTGGTGAG GGGATAACCA CTGCTATGAA AGGTAATGAT	GACGATACTT CTGCTATGAA		ATCCATAACA TGGCTCTTTG TAGGTATTGT ACCGAGAAAC	TGGCTCTTTG	CCACAACTAT
1361	CTCTATTGGC GAGATAACCG	CTCTATIGGC TATAIGCCAA GAGATAACCG ATATACGGTT	TACTCTGTCC TTCAGAGACT ATGAGACAGG AAGTCTCTGA	TTCAGAGACT	CICTATIGGO TATATGGGAA TACUCTGTOC TICAGAGACI GACAGGGACI CTGTATITITA ACAGGATGGG GTCCATTIAT GAGATAACGG ATATAGGGIT ATGAGACAGG AAGICTCTGA CTGTGCCTGA GACATAAAAA TGTCCTACGC CAGGTAAATA	CTGTATTTTT	ACAGGATGGG TGTCCTACCC	GTCCATTTAT

#### DCMV-II

-	TCGCGCGTTT AGCGCGCAAA	. GGGTGATGAC	PCMV-II TOGGGCGTTI CGGTGATGAG GGTGAAAACC TCTGACAGG GGAGGTCCCG GAGAGGCTCA CAGCTTGTCT AGGGGGGAA GCACTACTG CGACTTTTGG AGACTGTGTA CGTGGAGGGC CTCTGCGAG GTGAACAGA	por TCTGACACAT AGACTGTGTA	pCMV-II I GCAGCICCCG A CGICGAGGGC	GAGACGGICA CAGCIIGICI CICIGCCAGI GICGAACAGA	CAGCTTGTCT GTCGAACAGA	GTAAGCGGAT CATTCGCCTA
81	GCCGGGAGCA	GCCGGGAGCA GACAAGCCCG CGCCCTCGT CTGTTCGGGC	GOCGEGARA GACAAGOCG TCAGGEGEG TCAGGEGETG TTGEGEGETG TCGGGEGTG CTTAACTATG CGGCATCAGA GGGCCTCGT CTGTTGGEGG AGTCGCGGGG AGTCGCCCAC AGCGCCCAC AGGCCCAACC AGATTGATAC GGCGTAGTCT	TVAGGGGGGG TVAGCGGGTG TTGGGGGGTG TCGGGGCTGG CTTAACTATG CGGGATCAGA AGTCCGGGGG AGTCGGCGAC AACGGGCGAC GAGTTGATAG GCGGTAGTCT	TTGGCGGGTG	TCGGGGCTGG	CTTAACTATG	CGGCATCAGA
191	GCAGATTGTA	CTGAGAGTGC	GGAGAITGTA CTGAGAGTGG ACCATATGAA GCTTTTTGCA AAAGCCTAGG CCTCCAAAAA AGCCTCCTCA CTACTTCTGG GGTCTAACAT GACTCTCAGG TGGTATACTT CGAAAAAGGT TTTGGGATCC GGAGGTTTT TGGGAGGAGT GATGAAGACC	GCTTTTTGCA	AAAGCCTAGG TTTCGGATCC	CCTCCAAAAA	AGCCTCCTCA TCGGAGGAGT	CTACTTCTGG
241	AATAGCTCAG TTATCGAGTC	AGGCCGAGGC TCCGGCTCCG	AATACCTCAG AGGCGGAGG GCCTCGGC TCTGCATAA TAAAAAAT TAGTCAGCCA TGGGGGGAG AATGGGGGGA TTATCGAGTC TCGGGTCGG CGGAGGCGG AGACGTATT ATTTTTTTA ATCAGTGGG ACCGGCCTG TTACCGGCCT	TCTGCATAAA AGACGTATTT	TAAAAAAAT ATTTTTTA	TAGTCAGCCA	TGGGGCGGAG	AATGGGCGGA TTACCCGCCT
321	ACTGGGCGGG TGACCCGCCC	GAGGGAATTA CTCCCTTAAT	ACTGGGCGGG GAGGGAATTA ITGGCTATTG GCCATTGCAI ACCTTGTATC TATATCATAA TATGTACATT TATATTGGCT TGACGCGGCC CTCCCTTAAT AACGGATAAC GGGTAAGGTA TGCAACATAG ATATAGTATT ATACATGTAA ATATAAGGA	GCCATTGCAT	ACGTTGTATC TGCAACATAG	TATATCATAA ATATAGTATT	TATGTACATT ATACATGTAA	TATATTGGCT
401	CATGTCCAAT GTACAGGTTA	ATGACCGCCA TACTGGCGGT	CATGTCCAAT ATGACCGCCA TGTTGACATT GATTATTGAC TAGTTATTAA TAGTAATCAA TTAGGGGGTG ATTAGTTCAT GTACAGGTTA TAGTGGGGGT ACAAGTGTAA CTAATAACTG ATCAATAATT ATGATTAGTT AATGGCCCAG TAATCAAGTA	GATTATTGAC	TAGTTATTAA ATCAATAATT	TAGTAATCAA ATCATTAGTT	TTACGGGGTC	ATTAGTTCAT
481	AGCCCATATA TCGGGTATAT	TGGAGTTCCG ACCTCAAGGC	AGCCCATATA TGGACTICCG CETTACATAA CITACGETAA ATGGCCCGCC TGGCTGACG CCCAACGAC CCGGCCGTT TGGGGTATAT ACCTCAAGG GCAATGTAIT GAATGCCATI TACGGGCGG ACGGACTGC GGGTTGCTGG GGCGGGTAA	CTTACGGTAA	ATGGCCCGCC TGGCTGACCG TACCGGGCGG ACCGACTGGC	TGGCTGACCG	CCCAACGACC	CCCGCCCATT
561	GACGTCAATA CTGCAGTTAT	ATGACGTATG TACTGCATAC	GACGTCAATA ATGACGTATG ITCCCATAGT AACGCCAATA GGRACTITCC ATTGACGTCA ATGGGTGGAG TATTTACGGT CTGCAGTTAT TACTGCATAC AAGGGTATCA TTGCGGTTAT CCCTGAAAGG TAACTGCAGT TACCGACCTC ATAAATGCCA	AACGCCAATA TTGCGGTTAT	GGGACTTTCC	GGGACTITCC AITGACGICA AIGGGIGGAG IAITFACGGI CCCTGAAAGG IAACIGCAGI IACCCACCIC AIAAAIGCCA	ATGGGTGGAG TACCCACCTC	TATTTACGGT
641	AAACTGCCCA TTTGACGGGT	CTTGGCAGTA	CATCAAGTGT GTAGTTCACA	ATCATATGCC AAGTCCCCCC CCTATTGACG TCAATGAGGG TAAATGGCCC TAGTATACGG TTCAGGGGGG GGATAACTGC AGTTACTGCC ATTTACCGGG	AAGTCCGCCC TTCAGGCGGG	CCTATTGACG	TCAATGAGGG	TAAATGGCCC

FIG. 7-Page 1

8241	AGGACAGTAT TCCTGTCATA	TTGGTATCTG	AGGACAGTAT TIGGTATCTG GGCTCTGCTG AAGCCAGTTA CCTTGGGAAA AAGAGTTGGT AGCTCTTGAT CCGGCAAAGA ICCTGTCATA AACCATAGAC GCGAGAGGAC TICGGTCAAT GGAGGCTTT TICTCAAGCA TGGAGAACTA GGCGGTTTGT	AAGCCAGTTA TTCGGTCAAT	TA CCTTCGGAAA AT GGAAGCCTTT	OCTICGGAAA AACAGIIGGI AGCICIIGAI GGAAGCCIII ITCICAACCA ICGAGAACIA	AGCTCTTGAT TCGAGAACTA	CCGGCAAACA GGCCGTTTGT
8321	AACCACCCT TTGGTGGCGA	GGTAGCGGTG CCATCGCCAC	GTTTTTTGT CAAAAAAACA	TTGCAAGCAG	TIGGAAGGAG GAGATTAGGC GGAGAAAAA AGGATGTGAA GAAGATGCTT AAGGTIGGIC GTCTAATGGG GGTCTTTTTT TCCTAGAGTT CTTGTAGGAA	CAGATTACGC GCAGAAAAA AGGATCTCAA GTCTAATGCG CGTCTTTTT TCCTAGAGTT	AGGATCTCAA TCCTAGAGTT	GAAGATCCTT
8401	TGATCTTTTC ACTAGAAAAG	TGATCTTTC TACGGGGTCT ACTAGAAAAG ATGCCCCAGA	TGATCITIC TACGGGGTCT GACGCTCAGT GGAACGAAAA CTCACGTTAA GGGATTTTGG TCATGAGATT ACTAGAAAAG ATGCCCGAG CTGCGAGTCA CCTTGCTTTT GAGTGCAATT CCCTAAAACC AGTACTCTAA	GGAACGAAAA	GACGCTCACT GGAACGAAAA CTCACGTTAA GGGATTTTGG TCATGAGATT ATCAAAAAGG CTGCGAGTCA CCTTGCTTTT GACTGCAATT CCCTAAAACC AGTACTCTAA TAGTTTTTCC	GGGATTTTGG CCCTAAAACC	TCATGAGATT AGTACTCTAA	ATCAAAAAGG TAGTTTTTCC
8481	ATCTTCACCT TAGAAGTGGA	AGATCCTTTT TCTAGGAAAA	ATCTICACCI AGAICCITIT AAATIAAAAA IGAAGITITA AAICAAICIA AAGIAIAIAI GAGIAAAGIT TAGAAGIGGA ICIAGGAAAA ITIAAITITI ACITCAAAAI ITAGITAGAI IICAIAIAIA CICAITIGAA	TGAAGTTTTA	AATCAATCTA TTAGTTAGAT	AAGTATATAT GAGTAAACTT TTCATATATA CTCATTTGAA		GGTCTGACAG
8561	TTACCAATGC AATGGTTACG	TTAATCAGTG AATTAGTCAC	TYACCAATGC TTAATCAGTG AGGGACCTAI CTOAGGGATC TGTCTATTTC GTTCATCCAT AGTTGCCTGA CTCCCCGTCG AATGGTTAGG AATTAGTCAC TCCGTGGATA GAGTGGCTAG ACAGATAAAG CAAGTAGGTA TGAAGGAGT GAGGGGAGC	CTCAGCGATC	TGTCTATTTC ACAGATAAAG	GTTCATCCAT	AGTTGCCTGA TCAACGGACT	CTCCCCGTCG
8641	TGTAGATAAC ACATCTATTG	TACGATACGG ATGCTATGCC	TGTAGATAAC TACGATACGG GAGGGCTTAC CATCTGGCCC CAGTGCTCCA ATGATACGGC GAGACCGAGG CTCACGGGT ACATCTATTG ATGCTATGCC CTCCGGATG GTAGACGGG GTCACGACGT TACTATGGCG CTCTGGGTGG GAGTGGCGGA	CATCTGGCCC	CAGTGCTGCA	ATGATACCGC TACTATGGCG	GAGACCCACG	CTCACCGGCT
8721	CCAGATTTAT CAGCAATAAA GGTCTAAATA GTCGTTATTT	CAGCAATAAA GTCGTTATTT	GCAGATITAT CAGCAATAAA CCAGCCAGC GGAAGGGGGG AGGGCAGAAG TGGTGCTGGA ACTITATGGG CCTGCATGGA GGTGTAAATA GTGGTTATT GGTGGGTGGG CCTTGCGGGG TGGGGTCTTC ACCAGGAGGT TGAAATAGGG GGAGGTAGGT	GGAAGGGCCG	AGCCCAGAAG TGGTCCTCCA ACTITATCCG CCTCCATCCA TGGCGTCTTC ACCAGGACGT TGAAATAGGC GGAGGTAGGT	TGGTCCTGCA	ACTTTATCCG TGAAATAGGC	CTCCATCCA
8801	GTCTATTAAT CAGATAATTA	TGTTGCCGGG ACAACGGCCC	GICTAITAAT TOTTGCCGGG AAGGTAGAGT AAGTAGTICG COAGTTAATA GTTTGCGGAA GGTTGTTGCC ATTGCTAGAG CAGATAATTA ACAAGGGCC TTGGATGTGA TTGATGAAGG GGTGAATTAT CAAAGGGGTT GGAAGAAGG TAAGGATGTC	AAGTAGTTCG TTCATCAAGC	CCAGTTAATA	GTTTGCGCAA	CGTTGTTGCC /	ATTGCTACAG TAACGATGTC
8881	GCATCGTGGT	GTCACGCTCG	GOATICHGET GTCACGGTCG TGGTTTGGTA TGGCTTCATT CACCTCCGGT TGCCAACGAT CAAGGGGACT CGTACCACCA CAGTGCGAGG AGCAAACCAT ACGGAGGTAA GTGGAGGGCA AGGGTGGTA GTTCGGGTA	TGGCTTCATT	CAGCTCCGGT	TCCCAACGAT (AGGGTTGCTA)	SAAGGCGAGT 1	TACATGATCC ATGTACTAGG

FIG. 5-Page 15

7521	CGCATTGTCT GCGTAACAGA	CCCIANO DE PORTO CATTOTATIC TEGGGGGTGG GETGGGGGGG GACACCAAGGGGGTAACAGA CTCATCCACA GTAAGATAAG ACCCCCCACC CCACCCCGTC CTGTCGTTCC	CATTCTATTC	TGGGGGGTGG	TGG GGTGGGGCAG	GACTAGGTOT CATTCTAITC TGGGGGGTGG GGGGGGGG GACACCAAGG GGGAGGATTG GGAAGACAAT CTCATCCACA GTAAGATAAG ACGCCGCACC CAGCCGGTC CTGTGGTTCC CGCTCCTGAAG CGTTCTGTTA	GGGAGGATTG	GGAAGACAAT CCTTCTGTTA
7601	AGCAGGCATG	AGCAGGCATG CTGGGGAGCT CTTCGCCTTC CTGGCTCACT GACTGGCTGC GGTGGGTGCT TGGGCTGCG CGAGCGGTAT TGGTCGGTAC GACCGCTCGA GAAGGCGAAG GACGAGTGA CTGAGGGAGG CGAGCGAGGA GCGGAGGG GCTGGCGATA	CTTCCGCTTC	CTCGCTCACT	GACTCGCTGC	GCTCGGTCGT	TCGGCTGCGG	CGAGCGGTAT
7681	CAGCTCACTC	CAGCICACIO AAAGGCGGTA AIACGGITAI CCACAGAATC AGGGGATAAC GCAGGAAAGA ACATGTGAGC AAAAGGCCAG GTGGAGTGAG TITCGGCGAI TAIGGCAAIA GGTGTCTTAG TCGCCTATTG CGTGCTTTGT TGTACAGTGG TTTTCGGGTG	ATACGGTTAT	CCACAGAATC	AGGGGATAAC TCCCCTATTG	GCAGGAAAGA CGTCCTTTCT	ACATGTGAGC TGTACACTCG	AAAAGGCCAG TTTTCCGGTC
7761	CAAAAGGCCA GTTTTCCGGT	GAAAGGCCA GGAACCGTAA AAAGGCCGGG ITGCTGGCCT ITITCCATAG GGTCGCCCC CCTGACGAC AITACAAAA GTITCCGGT CCTTGGCATI ITTCGGGCG AACGACGCA AAAGGTAIC CGAGGCGGG GGATGCTCT TATTTTTT	AAAGGCCGCG TTTCCGGCGC	TTGCTGGCGT	TTTTCCATAG	AAAGGCGGG TIGCTGGCGT TITTCCATAG GCTCCGCCGC CCTGACGAGG ATGACAAAA TITCCGCGC AACGACGCG AAAAGGTATC CGAGGCGGGG GGACTGCTCG TAGTGTTTT	CCTGACGAGC	ATCACAAAA TAGTGTTTTT
7841	TCGACGCTCA AGCTGCGAGT	TOGACOCTCA ACTOAGAGGT GOCGAAACCC GACAGGACTA TAAACATACC AGGCGTTTCC CCCTGGAAGG TCCCTGGEG AGCTGCGACT TCAGTCTCCA CCGCTTTGGG CTGTCCTGAI ATTTCTATGG TCGGGAAAGG GGGACCTTGG AGGGAGCACG	GGCGAAACCC	GACAGGACTA	TAAAGATACC ATTTCTATGG	AGGCGTTTCC TCCGCAAAGG	CCCTGGAAGC	TCCCTCGTGC
7921	GCTCTCCTGT CGAGGGGCACA	CCTCTCCTGT TCCGACCTC CCGTTACC GATACCTGTC CGCCTTTCTC CCTTCGGGAA CCGTGGGGCT TTCTCAATGC CGAGGGGAA AGGTGGGAC GGGGAATGGC CTATGGACAG GGGAAGGC GGAAGCCCTT GGGCGGGA AAGAGTTAGG	CCGCTTACCG GATACCTGTC GCCGAATGGC CTATGGACAG	GATACCIGIC CTAIGGACAG	CGCCTTTCTC	CCTTCGGGAA	GCGTGGCGCT TTCTCAATGC CGCACCGCGA AAGAGTTACG	TTCTCAATGC
8001	TCACGCTGTA AGTGCGACAT		GGTATCTCAG ITCGGTGTAG GTCGTTCGCT CCATAGAGTC AAGCCACAIC CAGCAAGCGA	GTCGTTCGCT	CCAAGCTGGG	CCAAGCTGGG CTGTGTGCAC GGTTGGACCC GACACGTG	GAACCCCCG ITCAGCCCGA CITGGGGGG AAGTCGGGCI	TTCAGCCCGA
8081	CCGCTGCGCC	COCCTGCCCC TIATCCGCTA ACTATCCTOT TGAGTCCAAC CCGGTAAGAC ACGACTTATC GCCACTGCA GCAGCGACTGG GGCGCGCGG AATAGGCCAT TGATAGCAGA ACTCAGGTTG GGCGATTGTG TGCTGAATAG GGGTGACGGT GGTGGGTGA	ACTATCGTCT TGAGTCCAAC TGATAGCAGA ACTCAGGTTG	TGAGTCCAAC	CCGGTAAGAC	ACGACTTATC GCCACTGGCA TGCTGAATAG CGGTGACCGT	GCCACTGGCA	GCAGCCACTG
8161	GTAACAGGAT	OTANGAGGAT TAGGAGAGGG AGGTATGTAG GGGGTGCTAC AGAGTICTTG AAGTGGTGGG GTAACTAGGG CTAGAGTAGA GATTGTGCTA ATGGTGTGGG TGGARGATG GGGGGGAG TTGAGGAGG GATTGATGG GATGTGATGT	AGGTATGTAG TCCATACATC	AGGIATGIAG GCGGIGCIAC AGAGIICIIG ICCAIACAIC GCCCACGAIG ICICAAGAAC	AGAGTTCTTG TCTCAAGAAC	AAGTGGTGGC CTAACTACGG TTCACCACCG GATTGATGCC	CTAACTACGG GATTGATGCC	CTACACTAGA

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S P G B I N R V A A C L R K L G V P P L R A W R H R CTTCCAGGT GAATCAATA GGGTGGCGG ATGCCTCAGA AAACTTGGGG TACCGCCCTT GCGAGCTTGG AGACACCGGG GAGGCTCCA CTTTAGTTAT CCCACCGGG TACGGACTCT TTTGAACCC ATGGCGGGAA CGCTCGAACC TCTGTGGCCC	+2 A R S V R A R L L A R G G R A I C G K Y L F N W A V OVILL COCCEARCET CCCCCTAGG CTTCTGGCCA GAGGAGGCAG GGCTGCCATA GGGCCTGCA ACTCTTCAA CTGGCCACTA GGGCCTTCACA CGCGCCATCC GAAGAGGGGT CTCCTCCGTC CGCACGGTTA ACACCCTTCA TGGAGAAGTT GACCCCTCAT	R T K L K L T P I A A G Q L D L S G W F T A G Y S G AGAACAAACC TCAAACTCAC TCCAATAGGG GCCGCTGGCC AGCTCAACT GTCGGGTGG TTCAGGGGG GCTACAGGGG TCTTCAGGGG GCTACAGGGG TCGTTCTTCAGGGG GCATCAGGGG TCGACCTGAA CAGGCGGAGC AAGTCGCGA CAATGTGGC
+2 S P G E I N 6961 CTCTCCAGGT GAAATCAATA GAGAGGTCCA CTTTAGTTAT	+2 A R S V R A R 7041 CCCGGAGCGT CCGCGCTAGC	+2 R T K L K L T I T Z 121 AGACAAAGC TCAAACTCAC TCTTTTGG AGTTTGATTGATGGTG

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D E L GACGAACTCG CTGCTTGAGC
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- AAGGGGGTC GTAAGCCAGC TTCCCCCCAG CATTCGGTCG K N E V F C V O P E AAGAACGAGG TITICIGGGT TCACCCTGAG TTCTTGCTCA AAAGACGCA AGTCGACTC V T P I D T T I M A GLAACACCAA TAGACACTAC CATCATGGCT CATTGTGGTT GTGTGATG GTAGTACCGA
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- GTGGAAGTCC TCGTGCAAGC AGCACGTTCG GITGAAIICC CAACTTAAGG -----AATACTCACC AGGACAGGG TTATGAGTGG TCCTGTCGCC TGGCCGTGAT GGGAAGCTCC TACGGATTCC ACCGGCACTA CCCTTCGAGG ATGCCTAAGG 6081
- AGCGACATCC GTACGGAGGA TCGCTGTAGG CATGCCTCCT K K T P M G F S Y D T R C F D S T V T E AGGAAACC CAATGGGGTT CTCCTATGAT ACCGGTGC TTGACTCCA AGTGACTGA. TTCTTTTGG GTTACCCAA GAGCATACTA TGGGGGACGA AGTGAGGTG TCAGTGACT 6161
- TATGTTGGGG V A I K S L T E R L GTGGCCATCA AGTCCCTCAC CGAGAGGCTT CACGGGAGTG GCTCTCCGAA Q A R CCAAGCCCGC GGTTCGGGCG A I Y Q C C D L D P GGCAATCTAC CAATGTTGTG ACCTCGACCC CCGTTAGATG GTTACAACAC TGGAGCTGGG 6241

ATACAACCCC

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GAGGCCAACG CGGAGGATGT CICCGGIIGC GCCICCIACA CATGGTCAAC GGTCAGTAGT GACCICCCC TCGGACCCCT AGGCCTAGAA TCGCTGCCCA GTACCACTTG CCAGTCATCA CTGGAGGGG AGCCTGGGGA TCCGGATCTT AGCGACGGGT 5441

S M S Y S W T G A L V T P C A A E E Q K L P I TOANGICT ACTCTIGGAC AGGGCGCTC GTCCCCGT GGCCGCGCA AGAACACAAA CTGCCCATCA ACTTACAGAA TGAACACACT TGCGCGTCAC TCCTGCTT GACGGGTACT CGTGTGCTGC GCACACGACG ပ 5521

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AAAGTCACAT TTGACAGACT GCAAGTTCTG TTTCAGTGTA AACTGTCTGA CGTTCAAGAC 5681

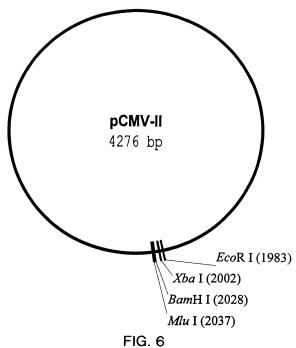
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P C E CCTTGCGAGC	R R L GCGAAGGTTG CGCTTCCAAC	CTTGCACCGC	I T R V ATCACCAGGG TAGTGGTCCC	I S V GATCTCCGTA CTAGAGGCAT	ACCCCCCCCT TGGGGGGCGA
S Q L GTCGCAATTA CAGCGTTAAT	A A G AGGGGCGG TCCGCCGGCC	L K A 1 CTCAAGGCAA GAGTTCCGTT	G G N GGGCGCAAC CCCGCCGTTG	ACGAGGGGA TGCTCGCCCT	P D Y N CCGGACTATA GCCTGATAT
L H E Y P V G S Q L P C E P D V A V L T S M L T D CTCACCAAT ACCGGTAGG GTGGGAATTA CCTTGGGAGC CCGAACGGGA GTGGGCGTG TTGAGGTCA TGGGGCTTCA TGGGCGATCC CAGGGTGACTG GGGGTGTTA TGGGCCATC CAGGGTGACTG GGCTTGGCCA TGGGCCATC CAGGGTGACT	42 P. S. H. I. T. A. E. A. G. R. R. L. A. R. G. S. P. P. S. V. A. S. S. S. A. C. S. CERCOCCAT. ATAACAGGG AGGCGGCGG GGGAAGGTTG GCGAGGGGAT CACCCCCTC TGTGGCCGGC TCTGGCTA TATTGTGCTC TCGGCGGCG GGCTTCCGATGCGTA TATTGTGCTC TCGGCGGCC GCTTCCCATA CGCTCCCCTA GTGGGGGGGA ACACGGTG AGGGCGAT	+2 S Q L S A P S L K A T C T A N H D S P D A E L I B A N 4881 GCCAGCTATC CGCTCGATG CTCAGGCCAAGGCCAAG GGGCCAAG GGGCCAAG GGGCCAAG GGGCGAAG GGGGCAAG GGGGGAAG GGGGGG	42 L L W R Q E M G G N I T R V E S E N K V V I L D S F D GAGGGAGAL GGGGGGGAAG ATCACCAGG TTGAGTGAG AAACAAAGTG GTGATTCTGG GTGCTTGGA GAGGATGGT GGGGGAGGT GGGGGAGGT TAGGGTGC AACTCAGTG GTGATTGTGG GAGGAAGGT GAGGGAAGGT	+2 P L V A E E D E R E I S V P A E I L R K S R R F A Q 5041 TCCCTTTGGGAA TCCTGGGAA TCTGGGGAA TCTGGGGAA TCGCCGAGG TGGCGGAG TTGGCCGAGG TGGGGGGGGGG	+2 A L P V W A R P D Y N P P L V E T W K K P D Y E P V V E T W C K R P D Y E P V V V E T W C CONTROLLED FOR A RECACTOR GENERAL ACCOUNT TIGGEOGGE C GEOTEMENT TEGGEOGGE TEGANAME C COALTAINER RECALLED FOR ACCACTOR GENERAL TEGGEOGGE TEGANOMY AND ACCOUNT ACCATOR TO THE TEGER TEGER TO THE TEGER TEGER TO THE T
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FIG. 5-Page 9

V H G C P L P P K S P V P P P R K K R T V V L T E GTCCATTGG CCCGTTCC ACCTCCAAGAAG TCCCCTCCTG TGCCTCCGC TCCGAAGAAG CGCACGGTG TCCTCACTGA CAGGTACCGA CGGCGAAGGAGG TCGAGGGTTTC AGGGGAGGACA ACGCATGGGG AGCCTTCTTC GCCTGCCACC AGGAGTGACT

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8961	CCCATGTTGT GGGTACAACA	GCAAAAAGC	GGTTAGCTCC	POMAY PORTIGITOT GCAAAAAAGG GGTTAGCTCC TTCGGTCCTC CAGAGCTAGG TTGGCCCCAG TGTTATCACT GGGTACAACA CGTTTTTCG CCAATGGAGG AAGGCAGGAG GTGAGGAACA GTCTTCATTC AACGGGCGTG AGAATAGTGA	PCM V TUELINGSO STC CGATCGTTGT SAG GCTAGCAACA	CAGAAGTAAG GTCTTCATTC	TTGGCCGCAG	TGTTATCACT ACAATAGTGA
9041	CATGGTTATG GTACCAATAC	GCAGCACTGC	ATAATTCTCT	CATGGTTATG GCACCACTGC ATAATTCTCT TACTGTCATG CCATGCGTAA GATGGTTTTC TGTGACTGGT GAGTACTCAA GTACCAATAC GGTGGTGACG TATTAAGAGA ATGACAGTAC GGTAGGGATT CTACGAAAAG ACACTGACCA CTGATGAGTT	CCATCCGTAA	GATGCTTTTC CTACGAAAAG	TGTGACTGGT ACACTGACCA	GAGTACTCAA
9121	CCAAGTCATT GGTTCAGTAA	CTGAGAATAG	TGTATGCGGC	CCAACTCAIT CTGAGAAIAG TGTAIGGGGC GACGAGITG CTCTTGCCCG GCGTCAAIAC GGGAIAAIAC CGCGCCACAI GGTTCAGIAA GACTCTIATC ACAIACGCCG CTGGCTCAAC GAGAAGGGGC CGCAGTTAIG CCCTATATG GGGCGCTCTA	CTCTTGCCCG	GCGTCAATAC	GGGATAATAC	CGCGCCACAT
9201	AGCAGAACTT TCGTCTTGAA	TAAAAGTGCT ATTTTCACGA	CATCATTGGA GTAGTAACCT	AGCAGAACTI TAAAAGTGGT CATGATTGGA AAAGGTTGTI GGGGGGGAA ACTGTGAAGG ATGTTACGGG TGTTGAGATG TGGTGTTGAA ATTTTGAGGA GTAGTAACGI TTTGCAAGAA GCGCGGTTI TGAGAGTTGC TAGAATGGGG ACAACTGTAG	CGGGGCGAAA	ACTCTCAAGG TGAGAGTTCC	ATCTTACCGC TAGAATGGCG	TGTTGAGATC ACAACTCTAG
9281	CAGTTCGATG GTCAAGCTAC	TAACCCACTC	GTGCACCCAA	CACITCGATG TAACCCACTC GTGCACCCAA CTGATCTTCA GCATCTTTA CTTTCACCAG GGTTTCTGGG TGAGCAAAAA GTCAAGCTAC ATTGGGTGAG CACGTGGGTT GACTAGAAGT GGAAGTGGTC GGAAGAGGC ACTGCTTTTT	GCATCTTTTA	CTTTCACCAG	CITICACCAG CGITICIGGG IGAGCAAAAA GAAAGIGGIC GCAAAGACCC ACICGIIIII	TGAGCAAAAA
9361	CAGGAAGGCA GTCCTTCCGT	AAATGCCGCA TTTACGGCGT	AAAAAGGGAA TTTTTCCCTT	CACGAAGCA AAATCCCCCA AAAAAGGGA TAAGGCCAAC ACGGAAATGT TGAATAGTCA TACTCTTCCT TTTTCAATAT GTCCTTCCGT TTTACGGCGT TTTTTCCCTT ATTCCCGCTG TGCCTTTACA ACTTATAA	ACGGAAATGT TGCCTTTACA	TGAATACTCA ACTTATGAGT	TACTCTTCCT	TTTTCAATAT AAAAGTTATA
9441	TATTGAAGCA ATAACTTCGT	TTTATCAGGG AAATAGTCCC	TTATTGTCTC AATAACAGAG	TATTCAACCA TITATCAGGG TIATTGTCTC ATGAGGGGAI ACATATTTGA ATGTATTTAG AAAAATAAAC AAATAGGGGT ATAACTTCGT AAATAGTCGC AATAACAGAG TACTGGCTA TGTATAAACT TACATAAATC TITITAITTG TITATCCCCA	ACATATTTGA TGTATAAACT	ATGTATTTAG TACATAAATC	AAAAATAAAC TTTTTATTTG	AAATAGGGT TTTATCCCCA
9521	TCCGCGCACA	TCCGCGCACA TTTCCCCGAA AACTGCCACC TGACGTCTAA AGCGCGCGTGT AAAGGGGCTT TTCACGGTGG ACTGCAGATT	AAGTGCCACC TTCACGGTGG		GAAACCATTA TTATCATGAC CITTGGTAAT AATAGTACTG	TTATCATGAC	ATTAACCTAT TAATTGGATA	AAAAATAGGC TTTTTATCCG
1096	GTATCACGAG CATAGTGCTC	GTATCACGAG GCCCTTTCGT CATAGTGCTC CGGGAAAGCA	ပဗ					

FIG. 5-Page 16

PCMV-deINS35  +2 I S E C T T P C S G S W L R D I W I C E V L S D D A CONTROL TARGETGGG GTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	FKTWLKAKLMPQLPGIPFVSCQRGYKG	TITAGGACT GGCIAAAAGC TAAGCICATG CGACAGCIGC CTGGGATCC CTTGTGTCC TGCCAGGGG GGTATAAGGG AAAITCIGGA CCGATITICG AITCGAGTAC GGTGTGGAG GACCTAGGG GAAAGAGAG ACGGTGGGG CGATAITCGC	+2 V W R G D G I M H T R C H C G A E I T G H V K N G T 4321 GGTTGGCGA GGGGACGACCA GGTTGGCAGCA GGGGACGACCA GGAGCGCT CCCTGGCGA GGATGACGGTGT AGTGCGAGCA CCAGACCGCT CCCTGGCGT AGTACGTGTG AGGGGGGTG AGACGCGCT CCTAGTGACCT CTAGTGACT TTGCCCTGCT	+2 M R I V G P R T C R N W S G T F P I N A Y T T G P C 4401 TCAGGATCGT GGGTCGTAGGA GGGCCCTGT ACTCGTAGGA GGGCCCTGT ACTCGTAGGA GGGCCCTGT ACTCGTAGGA GGGTCGTGT TGTAGGCT TGTAGGCT GGGGCGGGAGA	+2 T P L P A P N Y T F A L W R V S A E E Y V E I R Q V G A ACCCCTIC CIGGGGGGALA GCAGGGGGGGGGGGGGGGGGGGGGGGGGGG	+2 D F H Y V T G M T T D N L K C P C Q V P S P E F F T 4561 GGACTICCAC IACGICAGGG GTATGACTAC TGAGAATCTT AAATGCCCGT GCGAGGTCCC ATGGCCCGAA TTTTTCAAGGCCCC CCTAGAGGCTG ATGGAGTGCC CATAGTGATG ACTGTTAGAA TTTACGGGCA GGCGCGCTT AAAAAGGTGTC	+2 E L D G V R L H R F A P C K P L L R E E V S F R V G 4641 AATTGGACGG GGTGGGGCTA CATAGGTTG CGCCCCTG CAAGCCTTG TTGGGACG ACTAGATA AATAGGTTG CGCCCCTG CAAGCCCTTG TTGGGAAA ACTAGATA AATAGATA AATAGAAA AATAGAAA AATAGAAA AATAGAAA AATAGAAA AATAGAAA AATAGAAA AATAGAAA AATAGAAAA AATAGAAAAAAAA
PCMV-d <sub>1</sub> S G S W L R CTCCG GTTCCTGGCT AAGGG	L M P Q L P G	CATG CCACAGCTGC CTGGGAGTAC GACCC	H T R C H C G ACAC TGGCTGCAC TGTGG4 TGTG AGGGGGTG ACACCT	R N M W S G 1 AGGA ACATCTGGAG TGGGAG TGCT TGTACACCTC ACCCTG	F A L W R V CITIC GCGTAIGGA GGETGI	T T D N L K C CTAC TCACAATCTT AAATGC GATG ACTGTTAGAA TTTACG	F A P C K P
E C T T P C GGA GTGTACCACT CCATGC GCT CACATGGTGA GGTACG	TWLKAKI	CCT GGCTAAAGC TAAGCT GGA CCGATTTCG ATTCGA	R G D G I M CGA GGGACGCA TCATGC GCT CCCTGCCGT AGTACG	V G P R T C CGT CGTCTAGG ACCTGC GCAGGATCC TGGACG	T P A P N Y T FIC CIGCGCCGAA CTACACAAG	H Y V T G M ' AC TACGIGACGG GIATGA	G V R L H R
+2 I S S 4161 TAAGCTC	+2 F K 1	4241 TTTAAGAC AAATTCTC	4321 GGTCTGGC CCAGACCC	+2 M R I 4401 TCAGGATC ACTCCTAG	+2 T P L 4481 ACCCCCT TGGGGGA	+2 D F 4561 GGACTICC CCTGAAGG	+2 E L D 4641 AATTGGACU

FIG. 5-Page 8

1361	CTCTATTGGC	TATATGCCAA ATATACGGTT	PCMV-deiNS35 CICTATTGGC TATATGGGAA TACTGTGGC TTCAGAGACT GACAGGGACT CTGTATTTT GAGATAAGGG ATATAGGGTT ATGAGAGAGG AAGTCTGA CTGTGCCTGA GACATAAAA	pCM TTCAGAGACT AAGTCTCTGA	pCMV-delNS35 GACT GACAGGACT CTGA CTGTGCCTGA		ACAGGATGGG TGTCCTACCC	CTGTATTTTT ACAGGATGGG GTGCATTTAT GAGATAAAAA TGTGCTAGGC CAGGTAAATA
1441	TATTTACAAA ATAAATGTTT	TTCACATATA	TATTIACAAA ITCACATATA CAACAAGGC GICCCCGGG CCCGCAGITI ITAITAAACA IAGGGIGGGA ICTCCGACAI ATAAAIGTII AAGIGIAIAI GIIGTIGGGG CAGGGGGCAG GGGCGICAAA AATAAITIGI ATGGACCCT AGAGGCTGTA	GTCCCCCGTG	CCCGCAGITI	TTATTAAACA AATAATTTGT	TAGCGTGGGA	TCTCCGACAT AGAGGCTGTA
1521	CTCGGGTACG GAGCCCATGC	TGTTCCGGAC ACAAGGCCTG	CTCGGGTACG TOTTCCGGAC ATGGGCTCTT CTCCGGTAGC GGCGGAGCTT CCACATCCGA GCCCTGGTCC CATCCGTCCA GAGCCCATGC ACAAGGCCTG TACCCGAGAA GAGGCCATGG CGCCTCGAA GGTGTAGGCT GGGACCAGG GTAGGCAGGT	CTCCGGTAGC	GGCGGAGCTT	CCACATCCGA GGTGTAGGCT	GCCCTGGTCC	CATCCGTCCA
1601	GCGGCTCATG CGCCGAGTAC	GCGCTCATG GTCGCTCGGC CGCCGAGTAC CAGCGAGCCG	GGGGGTGATG GTGGGTGGG AGCTGCTTGC TGGTAAGAGT GGAGGGGAGA CTTAGGGAGA GGAGAATGGC CACCACGAG GGCGGGTAG GAGGGGGG TGGAGGAAGG AGGATTGTGA CCTGGGTGT GAATGCGTGT GFGTTAGGG GTGGTGGTGG	TCCTAACAGT	GGAGGCCAGA	AGCTCCTTCC TCCTAACACT GGAGGCCAGA CTTAGGCACA GCACAATGCC CACCACCACC TCGAGGAACG AGGATTGTCA CCTCCGGTCT GAATCGCTGT CGTGTTAGGG GTGGTGGTGG	GCACAATGCC	CACCACCACC
1681	AGTGTGCCGC TCACACGGCG	ACAAGGCCGT TGTTCCGGCA	AGTCTGCCGC ACAAGGCCGT GCGGTAGGG TATGTGTCTG AAATGAGCT CGGAGATTGG GCTCGCACCT GGACGCAGAT TAGAGGCGG TGTTCGGGGA CCGCCATCCC ATACACAGAC TTTTACTGGA GCCTCTAACC CGAGGTGGA CCTGCGTCTA	TATGTGTCTG	AAAATGAGCT TTTTACTCGA	CGGAGATTGG GCCTCTAACC	GCTCGCACCT	GGACGCAGAT
1761	GGAAGACTTA CCTTCTGAAT	AGGCAGCGGC TCCGTCGCCG	GGAAGACTTA AGGCAGGGG AGAAGAAGAI GCAGGCAGCI GAGTIGTICI ATICTGAIAA GAGTCAGAGG TAACTCGCGT CCTICIGAAT TCCGTCGCCG TCTTCTTCTA CGTCCGTCGA CTGAAGAAGA TAAGACTATT CTCACTCTCC ATTCAGGGCA	GCAGGCAGCT	GAGTIGTIGT CTCAACAACA	ATTCTGATAA TAAGACTATT	GAGTCAGAGG	TAACTCCCGT ATTGAGGGCA
1841	TGCGGTGCTG ACGCCACGAC	TTAACGGTGG AATTGCCACC	TECECTECT TIAACGITE AGGECACTOT AGTUTGACCA GTACTECTIG CTECEGEGE GECACCAGA CATAATAGET AGGECACGAC AATTGECACC TECEGTCACA TEAGACTECT CATGAGEAAC GAGGEGEGE GEGTGGTUT GTATTATEGA	AGTCTGAGCA TCAGACTCGT	GTACTCGTTG	CTGCCGCGCG	CGCCACCAGA	CATAATAGCT GTATTATCGA
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1921	GACAGACTAA CTGTCTGATT	CAGACTGTTC GTCTGACAAG	GACAGACTAA CAGACTGTTC CTTTCCATGG GTCTTTTCTG CAGTCACCGT CGTCGACCTA AGAATTCACC CTGTCTGATT GTCTGACAAG GAAGGTACC CAGAAAAGAC GTCAGTGGGG GCAGCTGGAT TCTTAAGTGG	GTCTTTTCTG	CAGTCACCGT	GCTCGACCTA	AGAATTCACC TCTTAAGTGG	ATGCCTGCAT TACCGACGTA

FIG. 5-Page 3

## SCOLULE VALUE

641	AAACTGCCCA TTTGACGGGT	AAACTGCCCA CTTGGCAGTA TTTGACGGGT GAACCGTCAT	CATCAAGTGT	PCMV-delNS35 AAACTGCCCA CTTGGCAGTA CATCATATGC AAGTCGCCC CCTATTGACG TCAATGAGG TAAATGGCCC TTTGACGGCT GAACGCTAT GTATTAGGG TTGAGGGGG GGATAACTGC AGTTACGGGG ATTTAGCGGG	pCMV-delNS35 AGGC AAGTCGGCCC AGGC TTCAGGCGGG	CCTATTGACG GGATAACTGC	TCAATGACGG AGTTACTGCC	TAAATGGCCC ATTTACCGGG
721	GCCTGGCATT	ATGCCCAGTA TACGGGTCAT	GCCTGGCATT ATGCCCAGTA CATGACCTTA		CGGGACTITC CTACTIGGCA GTACATCTAC GTATTAGTCA TCGCTATTAC GCCTGAAG GATGAACCGT CATGTAGAIC CATAATCAGT AGGCATAATG	GTACATCTAC	GTATTAGTCA	TCGCTATTAC
801	CATGCTCATG	GCCAAAACCG	AGTACACCAA TCATGTGGTT	CATGCTGATG COGITITIGGE AGTACACCAA TGGGCGTGGA TAGGGGTTTG ACTGAGGGGG ATTTCCAAGT CTCCACGCGA GTACCACTAC GCCAAAACG TCATGTGGTT ACGCGCACCT ATGGCGCAAAC TGAGTGGCCG TAAAGGTTGA GAGGTGGGG	TAGCGGTTTG	ACTCACGGG TGAGTGCCCC	ATTTCCAAGT	CTCCACCCCA
881	TTGAGGTCAA AACTGCAGTT	TGGGAGTTTG	TTTTGGCACC	TICACCICAA TOGGAGITIG TITIGGCACC AAAATCAACG GGACITICCA AAATGTCGIA ATAACCCCGC CCGTIGACG AACTGCAGIT ACCTCAAAC AAAACGGIGG ITITAGTIGC CCIGAAAGGI TITAGAGGAT TATGGGGGG GGGCAACTGC	GGACTTTCCA	AAATGTCGTA TTTACAGCAT	ATAACCCGC TATTGGGGCG	CCCGTTGACG
196	CAAATGGGCG GTTTACCCGC	GTAGGCGTGT CATCCGCACA	CAAATGGGCG GTAGGCGTGT ACGGTGGGAG GTCTATATAA STTTACCGG CATCGGCACA TGCCACCCTC CAGATATTT	CAAATGGGCG GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCG TTTAGTGAAC CGTCAGATCG CCTGGACACG GTTTACCGG CATCGGCACA TGCCACCCTC CAGATATATT CGTCTGGAGC AAATCACTTG GGAGTCTAGG GGACTCTGG	GCAGAGCTCG CGTCTCGAGC	TTTAGTGAAC	TTTAGTGAAC CGTCAGATCG CCTGGAGACG AAATCACTTG GCAGTCTAGC GGACCTCTGC	CCTGGAGACG
1041	CCATCCACGC	CCATCCACGC TCTTTTGACC TCCATACAAGGGTGCG ACTATCTTC	TCCATAGAAG	CCATCCACC TCTITIGACE TCCATAGAAG ACACCCGGAC CCATCCAGCC TCCCGGGCCG GGAACGGTGC ATTGGAACGC GTAGGTGCG ACAAAACTGG AGGTATCTTC TGTGGGCCTG GCTAGGTGCG AGGCGCGGG CCTTGCGAC TAACCTTGGG	CGATCCAGCC TCCGCGCCG GGAACGGTGC GCTAGGTCGG AGCCGCCGC CCTTGCCACG	TCCGCGGCCG	GGAACGGTGC	ATTGGAACGC TAACCTTGCG
1121	GGATTCCCCG CCTAAGGGGC	TGCCAAGAGT ACGGTTCTCA	GACGTAAGTA	GGAITCCCCG TECCAAGAGT GACCTAAGTA CCGCCTATAG ACTCTATAGG CACACCCCTT TGGCTCTTAT GCATGCTATA CCTAAGGGGC ACGCTTCTCA CTGCAITCAT GGGGGATATC TGAGATATCC GTGTGGGGAA ACCGAGAATA CCTACGATAT	ACTCTATAGG TGAGATATCC	CACACCCCTT TGGCTCTTAT GTGTGGGGAA ACCGAGAATA	TGGCTCTTAT	GCATGCTATA
1201	CTGTTTTTGG GACAAAAACC	CTTGGGGCCT	CTIGGGGCCI AIACACCCCC GCTCCTIAIG GAACCCCGGA IAIGIGGGG CGAGGAAIAC	CICITITIGG CITGGGGCCI AIACACCCCC GCTCCTIAIG CIAIAGGIGA IGGIAIAGCI TAGCCIAIAG CIGIGGGTIA GACAAAAACC GAACCCGGA TAIGIGGGGG CGAGGAAIAC GAIAICCACI ACCAIAICGA AICGCAIAIC CACACCAAI	CTATAGGTGA	TGGTATAGCT TAGCCTATAG ACCATATCGA ATCGGATATC	TAGCCTATAG	GTGTGGGTTA
1281	TTGACCATTA AACTGGTAAT	TTGACCACTC	TTGACCACTC CCCTATTGGT AACTGGTGAG GGGATAACCA	TICACCATTA ITGACCACIC CCCTATIGGT GACGATACIT TOCATTACIA AICCATAACA TGGCTCTITG CCACAACTAT AACTGGTAAT AACTGGTGAG GGGATAACCA CIGGTATGAA AGGTAATGAT TAGGTATIGT ACGGAGAAC GGTGTIGATA	TCCATTACTA	ATCCATAACA TGCCTCTTTG TAGGTATTGT ACCGAGAAC	TGGCTCTTTG	CCACAACTAT

FIG. 5-Page 2

	P L T T CCA CTAACCACTA GGT GATTGGTGAT
	T SACCAGO TEGETOGO
	CAGCIGCIGI
E *	TGGCTTTTA ACCGAAAAI
· · · · ·	TGCTTCATTG A ACGAAGTAAC T
T A T	ACCCCCCCAT
LPG	CTGCCTGGTA
L S T	CTTGTCAACG GAACAGTTGC
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T A F V TAC TGCCTTTGTG ATG AGGAAACAC	0
CG GTGCCGC	
C GCCCCCC	
TGCCCAGCT ACGGGTCGA	
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I L G CATATTGGGGG	
L F N CCTCTTCAAC	
S Q T L GCCAAACCCT CGGTTTGGGA	
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<sup>3761</sup> 

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G A L V GGAGCTCTTG CCTCGAGAAC	
G V A GGGCGTGGCG CCCGCACCGC	
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V G V V TCGGCGTGGT AGCCGCACCA	
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S P G CTCGCCCGGA GAGCGGGCCT	
P A I L CCGCCATCCT GCCGCTAGGA	
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R G CGGGGGA	
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A CCGCCTGATA	
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G A V Q W GGGCAGTGC AGTGGA CCCCGTCACG TCACCT	
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	H Q W CACCAGIGGA GIGGICACCI	
	R R L AGGCGACTC	
	T Q L L AA CCCAGCTCCT GA	
	L T V STCACTGE SAGTGACA:	
	L S S ACTCAGCAGC IGAGTCGTCG	
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	A A R V GCTGCCGGG TC CGACGGCGC AG	
	S D A A A R V T A I GAGCGATGCA GCTGCCCCC TCACTCCCAT, CTCGCTACGT CGACGGCCC AGTGACGCTA	
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81	GCCGGGAGCA	GCCGGGAGCA GACAAGCCC TCAGGGGGG TCAGCGGGTG TTGGCGGGTG TGGGGGCTGG CTTAACTATG CGGCATCAGA GGGCCTCGT CTGTTGGGG AGTCCGGGG AGTGGCCGAG AACGGCCAA AGCCCGAGC GAAITGATAG GCCTAGTGT	TCAGGGCGCG	TCAGCGGGTG	TTGGCGGGTG	TCGGGGCTGG	CTTAACTATG GAATTGATAC	CGGCATCAGA
161	GCAGATTGTA	SEUI  CGAGATIGIA CTGAGAGICG ACCAIAIGAA GCTITITIGGA AAAGCCTAGG CCTCGAAAAA AGCCTCGICA CTACTICTGG CGTCTAACAT GACTCTCACC TGGTATACIT GGAAAAAGGT ITICGGAICC GGAGGITITI TCGGAGGAGT GATGAAGACC	ACCATATGAA TGGTATACTT	GCTTTTTGCA	Stul AAAGCCTAGG C TTTCGGATCC G	II CCTCCAAAAA GGAGGTTTTT	AGCCTCCTCA TCGGAGGAGT	CTACTTCTGG
241	AATAGCTCAG TTATCGAGTC	AATACCTCAG AGGCCGAGGC GGCCTGGGC TCTGGATAAA TAAAAAAAT TAGTCAGCCA TGGGGCGGAG ATTGGGGGGA TTATGGAGTC TCGGGTCCG CGGGAGCGG AGACGTATTT ATTTTTTTA ATCAGTGGT ACCGCGCT TACCCGCCT	GGCCTCGGCC	TCTGCATAAA AGACGTATTT	TAAAAAAAT ATTTTTTA	TAGTCAGCCA	TGGGGCGGAG	ATTGGGCGGA
321	ACTGGGCGGG TGACCCGCCC	ACTGGGCGGG GAGGGAITA ITGGCTAITG GCCAITGCAI ACGTIGTATC IAIATCAIAA TAIGTACAIT TAIAITGGGT IGAGCGGGCG CICCCITAAI AACGGATAAC GGCAACGTA IGCAACATAG ATAIAGTAIT ATAGAIGTAA ATATAACGGA	TTGGCTATTG	GCCATTGCAT	ACGTTGTATC TGCAACATAG	TATATCATAA ATATAGTATT	TATGTACATT	TATATIGGCT
401	CATGTCCAAT GTACAGGTTA	CATGICCAAT ATGACGGCA IGITGACATI GATTATIGAC TAGITATAA TAGIAATCAA ITAGGGGGIC ATAGITGAT GTACAGGITA TAGIGGGGGI ACAAGIGIAA CIAATAAGIG ATCAATAAIT ATCAITAGII AATGGCCCAG TAATGAGTA	TGTTGACATT ACAACTGTAA	GATTATTGAC	ATGACCGCCA ICTICACATI CATTATICAC IACTIATAA TACTAATCAA TACTGCGCGT ACAACTGTAA CTAATAACTG ATCATAATI ATCATTAGTI	TAGTAATCAA	TTACGGGGTC ATTAGTTCAT AATGCCCCAG TAATCAAGTA	ATTAGTTCAT
181	AGCCCATATA TCGGGTATAT	AGCCATATA TGGACTICCO CCITACATA CITACCCTAA ATGGCCCCC TGGCTGACCG CCCAACGAC CCCGCCCAA ICGGGTATAT ACCTCAAGGC GCAATGTAIT GAATGCCAIT TACGGGCGCG ACCGACTGGC GGCTGGG GGGCGGTAA	CGTTACATAA GCAATGTATT	CTTACGGTAA	ATGCCCGCC	TGGCTGACCG	CCCAACGACC (	CCGCCCATT
191	GACGICAAIA CIGCAGIIAI	GACGICAAIA AIGACGIAIG ITCCCAIAGI AACGCCAAIA GGGACTITCC AITGACGICA AIGGGIGGAG IAITIACGGI CIGCACIIAI IACIGCAIAC AAGGGIAICA ITGCGGIIAI CCCIGAAAGG IAACIGCAGI IACCCACCIC AIAAAIGCCA	TTCCCATAGT	AACGCCAATA TTGCGGTTAT	ATCACCIATG TICCCATACT AACGCCAATA GGGACTITCC ATTCACCICA AIGGGTGGAG TATTTACGCT TACTGCATAC AAGGGTATCA TTGCGGTTAT CCCTGAAGG TAACTGCAGT TACCCACCTC ATAAATGCCA	ATTGACGTCA TAACTGCAGT	ATGGGTGGAG 1	TATTACGGT ATAAATGCCA

FIG. 5-Page 1

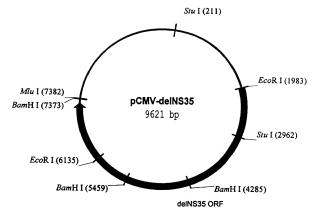


FIG. 4

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F K Q GTTCAAGCAG CAAGTTCGTC
L A E Q TCGCCGAGCA AGCGGCTCGT
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GCCICACTCA TATAGATGCC CACTITCIAI CCCAGAGAAA GCAGAGTGGG GAGAACCTIC CITACCIGGI AGCGTACCAA CGGAGTGAGI ATAICIAGGG GTGAAAGAIA GGGICIGTII CGICICAGCC CICITGGAAG GAATGGACGA ICGCATGGTI 2961

#### DCMV-NS35

				DG DG	pCMV-NS35			
8961	CCCATGTTGT GGGTACAACA	CCCATGTTGT GCAAAAAAGG GGITAGGTGC ITGGGTGCT CGGAGGTGT CAGAAGTAAG TIGGGGGGG IGTIATGACT GGGTAGAAGA GGTITITIGG GCAATGGAGG AAGGGAGGAG GCTAGGAAGA GFCITGAITG AAGGGGGGTG AGAATAGTGA	GGTTAGCTCC CCAATCGAGG	TTCGGTCCTC AAGCCAGGAG	CGATCGTTGT GCTAGCAACA	CAGAAGTAAG GTCTTCATTC	TTGGCCGCAG AACCGGCGTC	TGTTATCAC: ACAATAGTG
9041	CATGGTTATG GTACCAATAC	GATGGITATG GCAGCACTGG ATAATICICT TACTGTCATG CCATCGGTAA GATGCITITC TGTGACTGGT GAGTACTCAA GTACCAATAC CGTGGTGACG TATTAAGAGA ATGACAGTAC GGTAGGCAIT CTACGAAAAG ACACTGACCA CTCATGAGGT	ATAATTCTCT TATTAAGAGA	TACTGTCATG	CCATCCGTAA	GATGCTTTTC	TGTGACTGGT ACACTGACCA	GAGTACTCAA
9121	CCAAGTCATT GGTTCAGTAA	CCAACTCATT CTGAGAATAG TGTATGGGGG GACCGAGTTG CTCTTGCCCG GCGTCAATAG GGGATAATAG CGGGCGAGAT GGTTCAGTAA GACTCTTATG ACATAGGGGG GTGGCTCAAG GAGAAGGGG CGCAGTTATG CGCTATTATG GCGGGTGTA	TGTATGCGGC ACATACGCCG	GACCGAGTTG	CTCTTGCCCG	GCGTCAATAC	GGGATAATAC CCCTATTATG	CGCGCCACA
9201	AGCAGAACTT TCGTCTTGAA	AGCAGAACIT TAAAAGTGCT CATCATTGGA AAACGTCTT CGGGGCGAAA ACTCTCAAGG ATCTTACCGC TGTTGAGATC TCGTCTTGAA ATTTTCACGA GTAGTAACCT TTTGCAAGAA GCCCCGCTTT TGAGAGTTCC TAGAATGGCG ACAACTCTAG	CATCATTGGA GTAGTAACCT	AAACGTTCTT TTTGCAAGAA	CGGGGGGAAA	TAAAACTECT CATCAITGGA AAACETTCTT CEGESCEAAA ACTCICAAGE ATCTIACCEC TCTTGACATC ATTITCACGA GTAGTAACCT TITGCAAGAA GCCCGGTTT TGAGAGTICC TAGAATGEGG ACAACTCTAG	ATCTTACCGC TAGAATGGCG	TGTTGAGAT
9281	CAGTTCGATG GTCAAGCTAC	CACITCCATC TAACCCACTC CTGCACCCAA CTCATCTTCA GCATCTTTA CTTTCACCAG CGTTTCTGGG TGAGGAAAA GTCAAGCTAC ATTGGGTGAG CACGTGGGTT GACTAGAAGAT GAAAGTGGTC GCAAAGACCC ACTGGTTTTT	GTGCACCCAA CACGTGGGTT	CTGATCTTCA GACTAGAAGT	GCATCTTTA	CTTTCACCAG	CGITICIGGG GCAAAGACCC	TGAGCAAAAA
9361	CAGGAAGGCA GTCCTTCCGT	AAATGCCGCA TTTACGGCGT	AAAAAGGGAA TTTTCCCTT	TAAGGGCGAC ATTCCCGCTG	ACGGAAATGT TGCCTTTACA	AAAAAGGGAA TAAGGGCGAC ACGGAAATCI TGAATACTCA TACTCTTCCT TTTTCAATAT TTTTCCCTT ATTCCGCTG TGCCTTTACA ACTTATGAGT ATGAGAAGGA AAAGTTATA	TACTCTTCCT ATGAGAAGGA	TTTTCAATA: AAAAGTTAT
9441	TATTGAAGCA ATAACTTGGT	TATICAACCA ITIAICAGGG ITAITGICIC AIGAGGGGAI ACAIATITGA AIGTAITIAG AAAAATAAAC AAATAGGGGI ATAACIICGI AAATAGICGC AATAACAGAG TACICGCCIA IGTATAAACI IACATAAAIC ITITTAITIG ITTAIGGGGO	TTATTGTCTC AATAACAGAG	ATGAGCGGAT TACTCGCCTA	ACATATTTGA TGTATAAACT	ATGTATTTAG TACATAAATC	AAAAATAAAC TTTTTATTTG	AAATAGGGG TTTATCCCC
9521	TCCGCGCACA	TCCGCGCACA TITCCCCGAA AACTGCCACC TGACGTCTAA GAAACCAITA TTATCATGAC AITAACCIAT AAAAATAGGC AGGCGCGTGT AAAGGGGCTT TTCACGGTGG ACTGCAGAIT CTTTGGTAAT AATAGTACTG TAATTGGATA TITITATCCG	AAGTGCCACC TTCACGGTGG	TGACGTCTAA ACTGCAGATT	GAAACCATTA CTTTGGTAAT	TTATCATGAC AATAGTACTG	ATTAACCTAT TAATTGGATA	AAAAATAGG TTTTTATCC
1096	GTATCACGAG CATAGTGCTC	GTATCACGAG GCCCTTTCGT C	၁၅					

FIG. 3-Page 16

8241		TTGGTATCTG	AGGACAGTAT TIGGTATCTG CGCTCTGCTG AAGCCAGTTA CCTTGGGAAA TCCTGTCATA AACCATAGAC GCGAGACGAC TIGGGTCAAI GGAGGCTTT	AAGCCAGTTA TTCGGTCAAT	TTA CCTTCGGAAA	AAGAGTTGGT TTCTCAACCA	AAGAGTIGGI AGCICITGAI TICICAAGCA ICGAGAACIA	CCGGCAAACA GGCCGTTTGT
8321	AACCACCGCT TTGGTGGCGA	GGTAGCGGTG CCATCGCCAC	AACCACCGCT GGTAGCGGTG GTTTTTTTGT TTGCAACCAC CAGATTACGC GCAGAAAAA AGGATGTCAA TTGGTGGCGA CCATCGCCAC CAAAAAAAAA AAGGTTGGTC GTCTAATGCG CGTCTTTTTT TCCTAGAGTT	TTGCAAGCAG	GTITITITICI IIGCAAGCAG CAGAITACGG GCACAAAAAA AGGAICTCAA CAAAAAAACA AAGGIICGIC GICIAAIGCG CGICITITIT ICCIAGAGTI	GCAGAAAAA	AGGATCTCAA TCCTAGAGTT	GAAGATCCTT
8401	TGATCTTTTC ACTAGAAAAG	TGATCTTTTC TACGGGGTCT ACTAGAAAAG ATGCCCCAGA	TGATCITITO TACGGGGTCT GACGCTCACT GGAACGAAAA CTCACGTTAA GGGATTTTGG TCATGAGATT ATCAAAAAGG ACTAGAAAAG ATGCCCGGG CTGCGAGTCA CCTTGCTTTT GAGTGCAATT CCCTAAAACG AGTACTGTAA TACTTTTGG	GACGCTCAGT GGAACGAAAA CTGCGAGTCA CCTTGCTTTT	CTCACGTTAA	GGGATTTTGG	CTCACGTIAA GGGATTITGG TCATGAGATI ATCAAAAAGG GAGTGCAATI CCCTAAAACC AGTACTCTAA TAGTITITGC	ATCAAAAAGG TAGTTTTCC
8481	ATCTTCACCT TAGAAGTGGA	AGATCCTTTT TCTAGGAAAA	ATCITCACCT AGATCCTITT AAATTAAAAA TGAAGTITTA AATCAATCTA AAGTATATAT GAGTAAACTT GGTCTGACAG TAGAAGTGGA TCTAGGAAAA TITAATTITT ACTTCAAAAT TTAGTTAGAT TTCATATATA CTCATTGGA CCAGACTGTC	TGAAGTTTTA	AATCAATCTA TTAGTTAGAT	AAGTATATAT TTCATATATA	GAGTAAACTT	GGTCTGACAG
8561	TTACCAATGC AATGGTTACG	TTAATCAGTG AATTAGTCAC	TTACCAATGC TTAATCAGTG AGGCACCTAI CTCAGGGATC TGTCTATTTC GTTCATCCAT AGTTGCCTGA CTCCCCGTCG AATGCTTACG AATTAGTCAC TCCGTGGATA GAGTGGCTAG ACAGATAAAG CAAGTAGGTA TCAACGGACT GAGGGGCAGC	CTCAGCGATC	TGTCTATTTC ACAGATAAAG	GTTCATCCAT	AGTTGCCTGA TCAACGGACT	CTCCCCGTCG
8641	TGTAGATAAC ACATCTATTG	TGTAGATAAC TACGATACGG ACATCTATTG ATGCTATGCC		GAGGGCTTAC CATCTGGCCC CAGTGCTGCA	CAGTGCTGCA GTCACGACGT	ATGATACCGC GAGACCCACG TACTATGGCG CTCTGGGTGC	GAGACCCACG	CTCACCGGCT
8721	CCAGATTTAT GGTCTAAATA	CCAGATTTAT CAGCAATAAA GGTCTAAATA GTCGTTATTT	CCAGAITIAT CAGCAATAAA CCAGCCAGGC GGAAGGGCCG AGGGCAGAG TGGTCCTGCA ACTITATCG CCTCCATCCA GGTCTAAATA GTCGTTATTI GGTCGGTCGC CCTTCCCGGC TCGCGTCTTC ACCAGGACGT TGAAATAGGC GGAGGTAGGT	GGAAGGGCCG	GGAAGGCCG AGCCCAGAG TGGTCCTGCA CCTTCCCGGC TCGCGTCTTC ACCAGGACGT	TGGTCCTGCA	ACTTTATCCG TGAAATAGGC	CCTCCATCCA
8801	GTCTATTAAT CAGATAATTA	STCTATTAAT TGTTGCCGGG CAGATAATTA ACAACGCCC	GICTATTAAT ICTIGCCGGG AAGCIAGACI AAGTACTICG CCAGITAATA GITTGCGCAA CGTIGTIGCC ATTGCTAGAG CAGATAATTA AGAACGGCC TIGGAICTCA ITCAICAAG GGTCAATTAT CAAAGGCGTI GGAAGAAGG TAAGGAIGTC	AAGTAGTTCG TTCATCAAGC	CCAGTTAATA	GTTTGCGCAA	CGTTGTTGCC	ATTGCTACAG TAACGATGTC
8881	GCATCGTGGT	GCATCGTGGT GTCACGCTCG CGTAGCACCA CAGTGCGAGC	TCGTTTGGTA	TGGCTTCATT	CAGCTCCGGT TCCCAACGAT GTCGAGGCCA AGGGTTGCTA	TCCCAACGAT	CAAGGCGAGT TACATGATCC GTTCCGCTCA ATGTACTAGG	TACATGATCC

FIG. 3-Page 15

#### DCMV-NS35

7521	CGCATTGTCT GCGTAACAGA	GAGTAGGTGT CTCATCCACA		pCMV TGGGGGGTGG ACCCCCCACC	pCMV-NS35 CATICIAITC TGGGGGTGG GGTGGGGGAG GAGGAAGG GGGAGGATTG GGAAGAAAT GTAAGATAAG ACCCCCACC CCACCCCGTC CTGTGGTTGC CCTCCTGTTA	GACAGCAAGG	GGGAGGATTG	GGAAGACAAT CCTTCTGTTA
7601	AGCAGGCATG TCGTCCGTAC	CTGGGGAGCT GACCCCTCGA	CTTCCGCTTC	CTCGCTCACT	AOCAGOGATO CTGGGGAGCT CTTCCGCTTC CTCGCTCACT GACTCGCTGC GCTCGGTTCGT TCGGCTGCGG CGACCGGTAT TCGTCCGTAC CACCCCTCGA GAAGGGGAAG GAGCGAGTGA CTGAGCGACG CGAGCCAGCA ACCCGACGC GCTCGCCATA	GCTCGGTCGT	TCGGCTGCGG	CGAGCGGTAT
7681	CAGCTCACTC	AAAGGCGGTA TTTCCGCCAT	ATACGGTTAT TATGCCAATA	CCACAGAATC	CAGCICACTC AAAGGCGGTA AIAGGGTIAI CCACAGAATC AGGGATAAC GCAGGAAAGA ACAIGTGAGG AAAAGGCGAG GTGGAGTGAG TITCGGGAI TAIGGCAAIA GGTGICTIAG TCGCCIATIG CGTGCTITCT TGTAGACTGG TITTCGGGTG	GCAGGAAAGA	ACATGTGAGC AAAAGGCCAG TGTACACTCG TTTTCCGGTC	AAAAGGCCAG
7761	CAAAAGGCCA GTTTTCCGGT	GGAACCGTAA CCTTGGCATT	AAAGGCCGCG TTTCCGGCGC	TTGCTGGCGT	CAAAAGGCCA GGAACCGTAA AAAGGCCGGG TTGCTGGCGT TTTTCCATAG GCTCGGCCC CCTGACGAG ATCACAAAAA GTTTCGGGT CCTTGGCATT TTTCGGGGG AACGACGGA AAAAGTATC CGAGGCGGGG GACTGTCT TATCTTTT	GCTCCGCCCC	CCTGACGAGC	ATCACAAAAA TAGTGTTTTT
7841	TCGACGCTCA AGCTGCGAGT	AGTCAGAGGT TCAGTCTCCA	GGCGAAACCC	GACAGGACTA	TOGACGCTCA ACTCAGAGGT GGCGAAACCC GACAGGACTA TAAAGATACC AGGCGTTTCC CCCTGGAAGC TCCCTCGTGC AGCTGCGAGT TCAGTCTCCA CCGCTTTGGG CTGTCCTGAI ATTTCTATGG TCGGCAAAGG GGGACTTCG AGGAGCACG	AGGCGTTTCC TCCGCAAAGG	CCCTGGAAGC	TCCCTCGTGC
7921	GCTCTCCTGT CGAGAGGACA	TCCGACCCTG AGGCTGGGAC	GCTCTCCTGT TCCGACCTG CCGCTTACCG GATACCTCTC CGAGAGGACA AGCTGGGAC GCGAATGGC CTATGGACAG	GATACCTGTC	CGCCTTTCTC	CCTTCGGGAA	GCGTGGCGCT	TTCTCAATGC
8001	TCACGCTGTA AGTGCGACAT	GGTATCTCAG CCATAGAGTC	TTCGGTGTAG AAGCCACATC	GTCGTTCGCT	TICGGIGTAG GICCITICGCI CLAAGCIGGG CIGIGIGCAC GAACCCCCCG TICAGCCCGA AAGCCACAIC CAGCAAGCGA GGIICGACCC GACACACGT CITGGGGGC AAGICGGGCT	CTGTGTGCAC GAACCCCCCG GACACACGTG CTTGGGGGGC	GAACCCCCG	TTCAGCCCGA
8081	CCGCTGCGCC	TTATCCGGTA AATAGGCCAT	ACTATCGTCT TGATAGCAGA	TGAGTCCAAC	COCCTGCGCC TTATCCGGTA ACTATCGTCT TGAGTCCAAC CCGGTAAGAC ACGACTTATG GCCACTGGCA GCAGCCACTG GCCGAGGGG AATAGGCCAT TGATAGCAGA ACTCAGGTTG GGCGATTCTG TGCTGAATAG GGGTGACGGT CGTGGGTGAC	ACGACTTATC GCCACTGGCA TGCTGAATAG CGGTGACCGT	GCCACTGGCA	GCAGCCACTG
8161	GTAACAGGAT CATTGTCCTA	TAGCAGAGCG	GTAACAGGAT TACCACAGGG AGGTATGTAG GCGGTGGTAC AGAGTTCTTG CATTGTCCTA ATCGTCTCGC TCCATACATC CGCCACGATG TCTCAAGAAC	GCGGTGCTAC	GTAACACGAT TAGCAGAGCG AGGTATGTAG GCGGTGCTAC AGAGTTCTTG AAGTGGTGGG CTAACTACGG CTACAAGA CATTGTCTA ATGGTCTGG TCCATACATC GGCAGGATG TCTCAAGAAC TTCACGAGGG GATTGATGGC GATGTGATGT	AAGTGGTGGC CTAACTACGG TTCACCACCG GATTGATGCC	CTAACTACGG	CTACACTAGA

FIG. 3-Page 14

- M P P D A E S Y S M P P GACGCTGAGT CCTATTCCTC CATGCCCCCC CTGCGACTCA GGATAAGGAG GTACGGGGG
- Þ А M A z A w S S S 3 S G Ω S BamHI G д ш Ö ч +2
- CGGAGGATGT GAGGCCAACG CATGGTCAAC GGTCAGTAGT GTACCAGTTG CCAGTCATCA TCCCTCCCA AGCGACGGGT AGCCTGGGGA TCCGGATCTT GACCICCCC TCGGACCCCT AGGCCTAGAA CTGGAGGGG 5441
- V C C S M S Y S W T G A L V T P C A E E Q K L P I V CHORGOGO CONCOCCOCCA AGANGARA CIDECOCATEA CONCOCCATEA GRANARA CIDECOCATEA CARANGARA CIDECOCATEA CARANGARG AGANGARA CIDECOCATEA CARANGARG ATTACAGA TGARARAT FORCAGGOTA COCCOCCAGA CATACAGAG AGANGARA CATACAGAG ATTACAGA CATACAGAG ATTACAGA TGARARAT TO AGANGARA CATACAGAG ATTACAGA TGARARAT TO AGANGARA CATACAGAG ATTACAGA TACAGAG ATTACAGAG 42
- T S R S A C Q R Q K ACCTCACGCA GTGCTTGCCA AAGGCAGAAG TGGAGTGCGT CACGAACGGT TTCCGTCTTC Y S T GTATTCCACC CTACGICACC ACAAITIGGI GATGCAGTGG TGTTAAACCA N N × N A L S N S L ATGCACTAAG CAACTCGTTG TACGIGATIC GIIGAGCAAC +2 5601
- V K A A A S K GTTAAAGCAG CGGCGTCAAA CAATTTCGTC GCCGCAGTTT 7 5681
- TITGGITATG AAACCAATAC CIGACGCCC CACACICAGC CAAAICCAAG GITIAGGIIC S S TCGAACGICG GACTGCGGG GIGIGAGICG Ħ д AGCTTGCAGC A C V K A N L L S V E E AGTGAAGGCT AACTTGCTAT CCGTAGAGGA TCACTTCCGA TTGAAGGATA GGCATCTCCT 5761

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+2 G D I Y	CCCTCTGTAA ATAG

. L. P. N. R. CCTCCCCAA GATAGAGAT TGGGGTAAAC ACTCCGGCCT AAAAAAAAA AAAATCTAG AAAGGCGCGC GAGGGGGGTG GGAGGGTTG GCTACTTCCA ACCCCATTG TGAGGCGGA TTTTTTTTT TTTTTAGATC TTTCCCGCGC
AAAAAAAAA TTTTTTTT
ACTCCGGCCT TGAGGCCGGA
TGGGGTAAAC ACCCCATTTG
12 G I Y L L P N R 1 GENCTRACT CCTCCCCACC CANTGAGGT TGGGGTAAC ACTCCGGCT AAA CGTAGATGGA GGAGGGGTTG GCTACTCCA ACCCCATTG TGAGGGGGGA TTT
L P N CCTCCCCAAC GGAGGGGTTG
G I Y I GCATCTACC1 CGTAGATGGA
7281

# 7361 CAAGATATCA AGGATCCACT ACGCGTTAGA GCTGGGTGAT CAGCCTCGAC TGTGCGTTGT AGTTGCCAGC CATGTGTTGT GTTGTATGT TCCTAGGTGA TGAGGGTGG TAGAGAACA MluI BAMHI

TAAAATGAG GAAATTGCAT ATTTTACTC CTTTAACGTA
TTTCCTA ATAA AAAGGAT TATT
TIGECECTEC CECETECETT CETTGACECT GGAAGGTGEE ACTOCCACTG TECTTTCETA ATAAAATGAG GAAA AAGGGGGAGG GGGAAGGGAA
GAAGGTGCC AC
CCTTGACCCT GGGAACTGGGA C
ICC CCCTGCCTT CC
TTGCCCCTCC AACGGGGAGG
7441

6401	N T L AACACCCTCA TTGTGGGAGT	T C Y I CTTGCTACAT GAACGATGTA	K A R CAAGGCCGG GTTCCGGGCC	A A C I GCAGCCTGTC CGTCGGACAG	GAGCGCAGG	L Q D GCTCCAGGAC CGAGGTCCTG	N T L T C Y I K A R A A C R A A G L Q D C T M L V C G AAGACCTCA CTICTAGAT CAAGGCCGG GCAGCCTGTG GATCCATG TGACCATGC TGGTGTGTGTGTGTTGTGGTGTGTGTGTGTGTGTGT	V C G TCGTGTGG AGCACACCC
6481	D D L CGACGACTTA GCTGCTGAAT	V V I GTCGTTATCT CAGCAATAGA	C E S A GTGAAAGCGC CACTTTCGCG	G V Q GGGGTCCAG CCCCAGGTC	E D A A GAGGACGCC	S L R CGAGCCTGAG GCTCGGACTC	: D D L V V I C E S A G V Q E D A A S L R A F T E A M CGAGGACTRA GYCCTTATA GYCCTTATOR GAGGCTATA GAGGCATAGA CGCGGAGGC CGCGGGAGTC TGGGAGTC TGGGAAGTGC CTCCGATACT	E A M GAGCTATGA CTCCGATACT
+2 6561	T R Y S CCAGGTACTC GGTCCATGAG	A P P CGCCCCCT GCGGGGGGA	G D P I GGGGACCCC CCCTGGGGG	P Q P E CACAGA GIGITGITGCTCT	Y D L ATACGACTTG TATGCTGAAC	E L I 1 GAGCTCATAA CTCGAGTATT	+2 T R Y S A P P G D P P Q P E Y D L E L I T S C S S N V GS561 CCAGGTACTC GGCGCCCCT GGGACCCC CACAACCAAA ATACGACTTG GAGTCATAA CATCATGCTC CTCCAACCTG GCTCCAACCAG GGCGGGGGGA CCCCTGGGGG GTCTTGGTCT TATGCTCAAC CTCCAACTAT GAGTACAACAG GAGTTTGGAG	S N V CTCCAACGTG GAGGTTGCAC

+ 6641

A R M GCGAGGATGA CGCTCCTACT CGAGAGACA AGAAAACTG CAGCTAATTG TOGCTAGGG AAAATAATTA TGTTTGGC CAGACTGGG CCTCTGTGGT TGTGTGGG CTAGTTAG CAGCGATGG CTGTTGG CCTCTGTGT TGTGTGGGG GTGAGTAAG CACCGATGG TTGTATTAGT ACAAAGGGG GTGTGAAAG 7

I L M T HF F S V L I A R D Q L E Q A L D C E I Y G A A A A CASTICATE A CAGGING CARGOGARY TRACCAGGING TRACCAGGING A TRACCAGGING A A CAGGING GATGGOGAGA TRACCAGGING A A CAGGING CONTAINS A CAGGING CAGGING A CA +2 6801

+2 6881

4801	P S H TCCCTCCCAT AGGGAGGGTA	I T A ATAACAGCAG TATTGTCGTC	E A A G AGGGGCCGG	GCGAAGGTTG CGCTTCCAAC	A R G GCGAGGGGAT CGCTCCCCTA	S P P S CACCCCTC GTGGGGGGAG	+2 P S H I T A E A A G R R L A R G S P P S V A S S S A 4801 TOCOTOCOLT ATAACAGAG AGGCGCCG GCGAAGCTTG GCGAGGGGTA CACCCCCTC TGTGGCCGAG TCCTGGGCTA AGGGGGGTA TATTGTGGTC TCCGCGGGC GCGTTCCAAC GGTTCCCTA GTGGGGGGGG ACACCGGTGG AGGAGGCGAT	S S A TCCTCGGCTA AGGAGCCGAT
4881	S Q L S GCCAGCTATC CGGTCGATAG	A P S CGCTCCATCT GCGAGGTAGA	L K A CTCAAGGCAA GAGTTCCGTT	T C T A CITGCACCGC GAACGIGGCG	N H D TAACCATGAC ATTGGTACTG	S P D TCCCTGATG AGGGGACTAC	+2 S Q L S A P S L K A T C T A N H D S P D A E L I E A N 4881 GCCACCTATC CGCTCCATC CTCAAGGGAA CTTGCAGGG TAACCATGA TCCCCTGATG CTGAGGTAA GAGGGCAAC GGGTGATAG GCGAGTAG GAGTTCCGTT GAACGTGGG ATTGGTAGTG AGGGGAGTAC GACTCGAGTT	E A N AGAGGCCAAC TCTCCGGTTG
4961	L L W CTCCTATGGA	R Q E M GGCAGGAGAT CCGTCCTCTA	G G N GGGGGCAAC CCGCCGTTG	I T R T ATCACCAGGG TAGTGGTCCC	7 E S E TTGAGTCAGA AACTCAGTCT	N K V AAACAAAGTG TTTGTTTCAC	+2 L L W R Q E M G G N I T R V E S E N K V V I L D S F D 4961 CTCCTATGGA GCGGGGAGAC ATCACCTGGG TTGACTGAGA AAAAAGTG CTGATTCTGG ACTCCTTGGA GAGGATACCT CCGTCCTTGA CGGGGGGTTG TAGTGGTCC AACTCGACTT TTTGTTTCAC CACTAAGAC CGGGGGAGCT	S F D ACTCCTTCGA TGAGGAAGCT
5041	P L V TCCGCTTGTG AGGCGAACAC	A E E ] GCGGAGGAGG CGCCTCCTCC	D E R E ACGAGCGGGA TGCTCGCCCT	I S V GATCTCCGTA CTAGAGGCAT	PAE 1 CCCGCAGAAA GGGCGTCTTT	L L R K TCCTGCGGAA AGGACGCCTT	+2 P L V A E B D E R E I S V P A E I L R K S R R F A Q 5041 TCCGCTTGTG GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	F A Q TTCGCCCAGG AAGCGGGTCC
5121	A L P V CCTGCCGT GGGACGGGCA	W A R TTGGGCGCGG	P D Y P CCGGACTATA GCCCTGATAT	ACCCCCCT TGGGGGGGA	V E T AGTGGAGAGG TCACCTCTGC	W K K I TGGAAAAGC ACCTTTTCG	+2 A L P V W A R P D Y N P L V E T W K K P D Y E P P V SILL CCCTGCCCGT TIGGGCGCGG CGGACTAIA ACCCCCGCT AGTGAAAAGG TGGAAAAAG CGCAACTACGA ACCACCTAGG GGGACGGCGG GGCGTGATAIT TGGGGGGGGG ACCTCTGG ACCTTTTCG GGCTGATGCT TGGTGGACAC	P P V ACCACCTGTG TGGTGGACAC
+2 5201	V H G C GTCCATGGCT CAGGTACCGA	GCCGCTTCC CGGGCGAAGG	P P K ACCTCCAAAG TGGAGGTTTC	V H G C P L P P K S P P V P P R K K ST P OF COCCECTEC ACCTCCAAGAG TOCCCTCCTG TGGCTCGGC TGGGAAGAG CAGGGTTCT AGGGGGGGA AGGGGGG AGGCTTCTTC	TGCTCCGCC ACGGAGGCGG	R K K TCGGAAGAAG AGCCTTCTTC	+2 V H G C P L P P K S P P V P P P R K K R T V V L T E S201 GTCCATGGCT GCCGCTTCC ACCTCACTGA TCCTACTGA CGAAGAAG CGAAGGGTG TCCTCACTGA CAGGGTACCGA GGGGGAAGG TGGAGGGTG TCCTACTGA CAGGGTACCGA GGGGGAAGG TGGAGGTTTC AGGGGGGGA AGCGTACTCTC GCCTGCCACC AGGAGTGACT	L T E TCCTCACTGA AGGAGTGACT
5281	S T L ATCAACCCTA TAGTTGGGAT	S T A I TCTACTGCCT AGATGACGGA	TGGCCGAGCT ACCGCTCGA	A T R CGCCACCAGA GCGGTGGTCT	S F G S AGCTTTGGCA TCGAAACGGT	S S T GCTCCTCAAC	+2 S T L S T A L A E L A T R S F G S S T S G I T G D A T A T A T A T A T A T A T A T A T A	T G D ACGGGCGACA

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AACGGGACGA TIGCCCIGCT z V W R G D G I M H T R C H C G A E I T G H V K GGTCTGGCGA GGGGAGGGCA TCATGCAGAC TCGCTGCAG TGTGGAGCTG AGATCACTGG ACATCTGAAA CCAGACCGCT CCCTGCOGT AGTACGTGTG AGCGAGGTG ACACCTCGAC TCTAGTGACC TGTACAGTTT 4321

M R I V G P R T C R N M W S G T F P I N A Y T T G P C TOAGGATOTT COCTTOTAGG ACCTGCAGGA ACATGTGGAG TGGGACCTTC CCCATTAATG CCTACACAC GGGCCCCTGT ACTCCTAGGA GCCAGGATCC TGGACGTCCT TGTACACCTC ACCTGGAAG GGGTAATTAC GGATGTGGG CCCGGGGACA 4401

GTGGAGATAA GGCAGGTGGG CACCTCTATT CCGTCCACCC ы T P L P A P N Y T F A L W R V S A E E Y ACCCCCTIC CTGCGCGAA CTACACGTIC GCGCTATGGA GGCTGTCTGC AGAGGAATAC : TGGGGGGAAG GACGCGGTT GATGTGCAAG GCCGATACCT CCCACAGAGG TCTCCTTATG 4

TTTTTCACAG AAAAAGTGTC GGACTICCAC TACCTGACGS CTATGACTAC TGACATGA TAAGTGCCGCT CCAGGTCC ATGGCCCGAA CCGAAGGTCC ATGGCCCAA ATGGCCAA ATGGCCCAA ATGGCCAA ATGGCCAA ATGGCCAA ATGGCCAA ATGGCCCAA ATGGCCAA ATGGCCCAA ATGGCCCCAA ATGGCCCAA ATGGCCCAA ATGGCCCCAA ATGGCCCAA ATGGCCAA ATGGCAA ATGGCCAA ATGGCAA ATGGCCAA ATGGCCAA ATGGCCAA AT G Н + 4561

E L D G V R L
AATTGGACGG GGTGCGCCTA
TTAACCTGCC CCACGCGGAT 4 1997

 $^{\rm P}$  C E  $^{\rm P}$  E P D V A V L T S M L T D CTITGGGGG C CGAACGGG CCTGGCCCT TTCACTCA TCTCACTCA GGAACGCTC GCCTTGGCCT GCACCGGCAC AACTGCAGT ACCACTGACT L H E Y P V G S Q L CTCCACGAAT ACCCGGTAGG GTCGCAATTA CAGCGTTAAT GAGGTGCTTA TGGGCCATCC

A F V TGCCTTTGTG ACGGAAACAC	3 Y G A GGTATGGCGC CCATACGGCG	N L L AATCTACTGC TTAGATGACG	P G E CCCGGGCGAG GGGCCCGCTC	V P E ACGTGCCGGA TGCACGGCCT	H Q W CACCAGIGGA GIGGICACCI	L S D STTGAGGGAC
G A A T GTGCCGCTAC CACGGCGATG	G A G L A G A I G S V G L G K V L I D I L A G Y G A GOCCTCGCT TAGGIGG COCCTGCGC GCCCTGCGC AGTCTTCGAC GCTATCGCC CCGCCACCGA ATCACCGC GCGCTAGCC TCACACCT TAGGACTCTC TAGGAACGT CATACCGCG	D L V GGACCTGGTC CCTGGACCAG	I L R R H V G P G E ATACTGGGC GGCACGTTGG CCGGGGGAG TATCACGCG CCGTCCACC	G A V Q W M N R L I A F A S R G N H V S P T H Y V P E GEGGGGTGC AGTGTTTCC CCA,GGGGGAA AGTGCGGGGAA CATGTTTCC CCA,GGGACT AGTGCCGGGGAA CCATGTTTCC CCA,GGGACT AGTGCCGGGGAA CGATGTTTCG CCA,GGGGCT TGGAGGGCGTA TGGAGGGGAA GGGGGCGTA TGGAGGGCGTA TGGAGGGCGT TGGAGGGCGT TGGAGGGCGTA TGGAGGGCGT TGGAGGGCGTA TGGAGGGCGT TGGAGGGCGTA TGGAGGGCGT TGGAGGGCGT TGGAGGGGGGGGGG	A A R V T A I L S L T V T Q L L R R L H Q W GCTGCCCGCG TCACTGCAL ACTCACAGCTCTA CCCACTCCT GAGCCACTG CACCAGTGGA CACGCGCGC AGTGACGCTA TGACTGCTG GAGTCGACAT GGGTCGACGA CTCCGCTGAC TGACTCGTCG CACTCACATT GGGTCGACGA CTCCGCTGAC TGACTCACATT GGGTCGACGA CTCCGCTGAC TGACTCACATT CACTCACATT	C E V TATGCGAGGT (ATACGCTCCA (
A A P GCCCCCCC CGCCGCGCC	L I D CCTCATAGAC GGAGTATCTG	P S T E CCTCCACGGA GGAGGTGCCT	I L R F ATACTGCGCC TATGACGCGG	H V S CCATGTTTCC GGTACAAAGG	Q L L CCCAGCTCCT GGGTCGAGGA	W D W I TGGGACTGGA
A Q L TGCCCAGCTC ACGGGTCGAG	L G K V TGGGGAAGGT ACCCCTTCCA	G E V ) GGTGAGGTCC CCACTCCAGG	P A I L S P G A L V V G V C A A COCCCATICAT CTGCCGCA GCCCTCGTAG TCGGCGTGT CTGTCCACA GCCGGTAGA GAGGGGCCT CGGGAGCATC AGCCGCACCA GACAGGTCGT	R G N CCCGGGGGAA GGGCCCCTT	L T V T CTCACTGTAA GAGTGACATT	R D I AAGGGACATC TTCCCTGTAG
G W V A GGTGGGTGGC CCACCCACCG	S V G AGTGTTGGAC TCACAACCTG	I M S GATCATGAGC CTAGTACTCG	7 G V V TCGGCGTGGT AGCCGCACCA	A F A S GCCTTGGCCT CGGAAGCGGA	L S S ACTCAGCAGC TGAGTCGTCG	S W L GTTCCTGGCT CAAGGACCGA
I L G ATATTGGGG TATAACCCC	A I G CGCCATCGGC GCGGTAGCCG	V A F K TGGCATTCAA ACCGTAAGTT	A L V CGCCTCGTAG	R L I CCGGCTGATA GGCCGACTAT	T A I TCACTGCCAT AGTGACGGTA	P C S G CCATGCTCCG GGTACGAGGC
CCTCTTCAAC GGAGAAGTTG	L A G A TAGCTGGCGC ATCGACCGCG	G A L GGAGCTCTTG CCTCGAGAAC	S P G CTCGCCGGA GAGCGGGCCT	W M N AGTGGATGAA TCACCTACTT	A A R V GCTGCCGGG CGACGGGGGC	C T T GTGTACCACT CACATGGTGA
+2 S Q T L L F N I L G G W V A A Q L A A P G A A I A F V S Q E COCAMACCT COTOTTCAAC ATAITGGGG GGTGGGTGGC TGCCTTTGTG CGTTTGGGA GGAGAAGTTG TATAACCCC CCACCLACCG GGGGGGGGGGGGGGGGGGGGGG	+2 G A G L A G A A I G S V G L G K V L I D I L A G Y G A GOOGCTGGCT TAGCTGGCG CGCCATCGCG AGTGTTGGAC TGGGGAAGGT CCTCATAGAC ATCCTTGGAG GCTATGGCGC CGGGAGCGCGA ATCGACGCG GGGGTAGCGC TGACAGCTG ACCCTTCCA GGACATCTC TAGGAAGGTC CCATACGGG	+2 G V A G A L V A F K I M S G E V P S T E D L V N L L SGEGETGEGE GAGCTICTTE TGGGATTCAA GATCATGAG GGGGTGGG GAGCTGGT AATCTACTGC CCCGCACCGC CCTCGAGAAC ACGGTAAGTT CTAGTACTGC CCACTCCAGG GGACTGCT CCTGGACAGG TAGATGACG	+2 P A I L S P G A L V V G V V C A A I L R R H V G P G E STANDER COCCONTICAT CTGGCCCATCA GARACTICG CCGACCATCA GGCCGCCAG GCCGCCAG GGCCGCCAG GGCCGGCC	42 G A V Q W M N R L I A F A S R G N H V S P T H Y V P E GOOGEGAGIGG AGGGGGGAA CCATGTTTCC CCCACCCAT ACGTCCCCA CCCGTCATA CCCTTCATA CCCTTCATC CCCACCCAT ACGTCCCCT CCCCGTCATC CCCACCCTAT ACGTCCCCT CCCGTCATCATCACG CCCTCATA CCCACCCCT CCCACCCCT CCTACAAGG CCCTCATA CCAACCCCT CCCACCCCT CCTACAAGG CCCTCATA CCAACCCCT CCACCCCT CCTACAAGG CCCTCATA CCAACCCCT CCAACCCCT CCTACAAGG CCCTCATA CCAACCCCT CCAACCCCT CCTACAAGG CCCTCATA CCAACCCCT CCAACCCCT CCAACCCCT CCAACCCT CCAACCCCT CCAACCCT CCAACCCCT CCAACCCT CCAACCCT CCAACCCCT CCAACCCT CCAACCAA	42 S D A A A R V T A I L S L T V T Q L L R R L H Q W 4081 GAGCGATGGA GCTGCCGGG TCACTGGA CCTGAGTGTA CCLAGCTGCT GAGCGACTG CACCAGTGGA CTGCGTGACGT CACCAGTGGA CTGCGTGAGG CTGCGTGAGG CTGCGTGAGGAGGA CTCGGTGAGG TGAGTGAGGTA TGAGTGAGATI GGGTGAGGAGA CTCGGTGAG CTGCGGTGAG CTGCGGTGAGGAGGA CTCGGTGAGGAGGA CTCGGTGAGGAGGA CTCGGTGAGGAGGA CTCGGGTGAGGAGGA CTCGGTGAGGAGGA CTCGGGTGAGGAGGA CTCGGGTGAGGAGGAGGA CTCGGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	+2 I S E C T T P C S G S W L R D I W D W I C E V L S D AGGEGATO TEGGACTEGA TATECCAGGT GITGAGGGG TTGGAGCTG TATEGGAGGT GITGAGGGG GITGAGGGG GITGAGGGG GAGGGGGG GAGGGGGG GAGGGGGG GAGGGGGG
3681	3761	3841	3921	4001	4081	4161

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V V T AGGTCGTCAC GA ICCAGCAGTG C1	
A D L E GCCGACCTGG AG CGGCTGGACC TC	
C M S ATGCATGTCG C TACGTACAGC C	
Y I M T C M S / ACATCATGAC ATGCATGTCG GC TGTAGTACTG TACGTACAGC CC	
3201	

K P A I I P D AAGCCGCAA TCATACCTGA TTCGGCCGTT AGTATGGACT A A Y C L S T G C V V I V G R V V L S G GCCGGGATATT GCCTGTGAAG AGGCTGGG GTCATAGTGG GGAGGGTGGT CTTGTCGGG GGGCGCATAA GGGACAGTTG TCCGAGGGCCC GAGTAGACA GAGAGGGCCC 4

CATCGAGCAA GGGATGATGC GTAGCTCGTT CCCTACTACG L Y R E F D E M E E C S Q H L P Y I E Q CTCTACCGAG ACTTACCATGA GATGGAAGAG TGCTCTCAGC ACTTACCCTA GATCCACAA GAGATGC TCAACTGCTC TCAACTTCT CTACCTTCTC ACGAGAGTCG TGAATGGCAT GTAGCTCTT CAGGGAAGIC GTCCCTTCAG ы

R Q A E V I A P A V CGTCAGGCAG AGGTTATCGC CCCTGCTGTC GCAGTCGTC TCCAATAGCG GGGACGACAG L A E Q F K Q K A L G L L Q T A S TCCCCAGCA GTTCAAGCA AAGGCCTCC GCCTCCTGCA GACCGCGTCC AGCGGCTCGT CAAGTTCGTC TTCCGGGAGC CGGAGGACGT CTGGCGCAGG 7 3441

Q I N W Q K L E I F W A K H M W N F I S G I Q Y L A C ACACACAGE GECAACAGE GEGAACI CGAGACTIC IGGGGGGG GICIGGTIG GCAINGAI ACITGGGGGG GICIGGTIG GCCITITICA GCICIGGAGG ACCGGCTICG IAIACACIT GAAGIACICA CCCITITICA GCICIGGAAG ACCGGCTICG IAIACACCTI GAAGIACTCA CCCIAIGIIA IGAACCGCCC 3521

CTAACCACTA L S T L P G N P A I A S L M A F T A A V T S P CTTGTCAACG CTGCCTGGTA ACCCCCCA TGCTTCATTG ATGGCTTTA CACCTGCTC CACGGCCA GACACTTGC GACGGACCAI TGGGGCGGTA ACGAAGTAAC TACCGAAAAT CTCGACGACA GTGGTCGGGT 3601

GATTGGTGAT

FIG. 3-Page 6

GCTGTCTCC CGACAGAGGG > CCCCCAAGAT GGGGGTTCTA 0 V T Q T V D F S L D P T F T I E T I T I T T TOTCACCCAG ACACTCGAT TCAGCCTICA CCCTACCTIC ACATTCAGA CAATCAGCT ACAGTGGGAC TGCTAACTCT GTTACTGCGA 2641

CATCTACAGA T G R G K P G ACTGGCAGG GGAAGCCAGG TGACCGTCC CCTTCGGTCC R T Q R R G R GCACTCAACG TCGGGGCAGG AGCCCCGTCC CGTGAGTTGC 2721

TGCGGGGGG TCTGATGTCA ACCCCCCCC ACACTACAGT ы M F D S S V L C E C Y D A G C A W Y E L ATGTICAACT CETCCGTCCT CTGTGACTGC TATGACGCGAG GCTGTGCTTG GTATGACGTC TACAAGCTGA GCAGGGA GACACTCACG ATACTGCGTC CGACAGGAAC CATACTCGAG 2801

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StuI GTCTTTACAG CAGAAATGTC TTGGGAGGGC AACCCTCCCG ATCTTGAATT TAGAACTTAA TGCCAGGACC ACGGTCCTGG GCTTCCCGTG CGAAGGGCAC ACACCCGGG TGTGGGGCCC GCGTACATGA CGCATGTACT TAGGCTACGA (ATCCGATGCT) 2881

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CTTACCTGGT AGCGTACCAA GAATGGACCA TCGCATGGTT GAGAACCTTC GCAGAGTGGG (CGTCTCACCC ( GCCTCACTCA TATAGATGCC CACTTTCTAT CCCAGACAAA CGGAGTGAGT ATATCTACGG GTGAAAGATA GGGTCTGTTT 2961

 $^{\rm P}$   $^{\rm P}$  S  $^{\rm W}$  D Q M W K C L I R  $^{\rm L}$  K P T CCCCATCCT GGACCAGAT GTGAAGTGT TTGATTCGC TGAAGCCAG GGGGTAGCA CCCTGGTCTA CACCTTCACA AACTAAGCG AGTTCGGGTG A T V C A R A Q A P GCCACCGTGT GCGCTAGGGC TCAAGCCCCT AGTTCGGGGA CGGTGCCACA CGCGATCCCG 3041

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	C H S T D A GIGCCACTCC ACGGATGCCA CACGGIGAGG IGCCTACGGT
	D I I C D E SACATAATAA TITGIGAGGA SIGIAITATI AAACACIGCI
	G A Y GGCGCTTAT
	A D G G C S G GCCGACGCG GGTGCTCGGG ( CGGCTGCCGC CCACGAGCCC (
	K F L CAAGTTCCTT
•	2161

T S I L G I G CATCCATCTT GGGCATTGGC GTAGGTAGAA CCCGTAACCG 2241

GACGAACTCG CTGCTTGAGC м K A I P L E V I K G G R H I I F C H S K K K C GARGGTATC COCCUTCAAA TAATCAAGGG GGGAAGAAT CTCATCATCAT CTGATTATCAAGAGAGGG GGGAAGAAC AGTAAGAT CTGTTTAAG GAGTAGAAGA CAGTAAGAT CTGTTGAAG

G I N A V A Y Y R G L D V S V I P T S G GEGATCANTG COSTGECCTA CTACGGGGT CTTGACGTCT CCGTCATCCC GACCAGGGG CCGTAGTAGG GGCACGGGAT GATGGCGCA GAACTGCACA GGCAGTAGGG CTGGTCGCCG A A K L V A L CCGCAAAGCT GGTCGCATTG GGCGTTTCGA CCAGCGTAAC 2481

D V V V V A T D A L M T G Y T G D F D S V I D C N T C GATGITGTGG TICGGGAAC CGATGCCGCC ATACCGGCGA CTTCCACTCG GTGATAGACT GCAATAGCGC CTACAGCGGTG GTTACGGGGA CTTCCACTCG CTGATAGACT GCAATAGCGAC GTACGGGGAG TACTGGCCGT GAAGCTGAGC CACTATGGCAAC 2561

FIG. 3-Page 4

#### DCMV-NS35

1441		PCMV-NS35 TATTAGAAA TTGAGATAA GAGAAGGG GTGCGCGGG GCGGAGTTT ATAAATGTTT AAGTGTATAT GTTGTTGGG GAGGGGGGA GGGCGTGAAA	CAACAACGCC	DCMV-NS35 CAACAACGC GTCCCCGTG CCCCAGTTT TTATTAAACA TAGGGTGGGA TCTCCGACAT GTTGTTGCGG CAGGGGGCA GGCGTCAAA AATAATTTGT ATGGACGCCT AGAGGCTGTA	PCMV-NS35 SCGTG CCCGCAGTTT SCCAC GGCCGTCAAA		TAGCGTGGGA	TTATTAAACA TAGGGTGGGA TCTCGGACAT AATAATTTGT ATGGCACCCT AGAGGCTGTA
1521		CTCGGCTACG TOTTCCGGAG ATGGGGTCTT CTCCGGTAGC GGGGGGCTT CCACATCGGA GCCTGGTCC CATCCGTCGA GAGCCCATGC ACAAGGCCTG TACCCGAGAA GAGGCCATGG CGCCTCGAA GGTGTAGGCT GGGGACGAGG GTAGGCAGGT	TGTTCCGAAC ATGGCCTCTT CTCCGGTAGC GGCGGAGCTT CCACATCCGA GCCCTGGTCC CATCCGTCCA ACAAGGCTG TACCGGAGA GAGGCCATGG CGCCTCGAA GGTGTAGGCT GGGAGCAGG GTAGGCAGGT	CTCCGGTAGC	GGGGGAGCTT	CCACATCCGA	GCCTGGTCC	CATCCGTCCA
1601	- 0	GCGCCTATG GTGCGTCGC AGCTCCTTGC TCCTAACAGT GGAGGCCAGA CTTAGGCACA GCACAATGCC CACCACCAC CGCGGAGTAC CAGGGAGCG TCGAGGAACG AGGATTGTCA CCTCGGGTCT GAATCCGTGT GGTGTTAGGG GTGGTGGTG	AGCTCCTTGC TCGAGGAACG	TCCTAACAGT	GGAGGCCAGA	CTTAGGCACA	GCACAATGCC	CACCACCACC
1681		AGIGIGCOGO ACAAGGCOGT GGCGCTAGGG TATGTGTCTG AAAATGAGCT CGGAGATTGG GCTCGGAGCT GGAGGGAGAT TAGAGGGG TGTTCGGGG CGGCGTCCC ATAGAGAGC TTTTAGTGGA GCCTCTAAGC GGAGGGTGGA CCTGGGTGTA	GGCGGTAGGG	TATGTGTCTG	AAAATGAGCT TTTTACTCGA	CGGAGATTGG	GCTCGCACCT	GGACGCAGAT
1761	GGAAGACTTA CCTTCTGAAT	GGAGACTTA AGGCAGGGG AGAAGAAGAT GCAGGCAGCT GAGTIGTTGT ATTCTGATAA GAGTCAGAGG TAAGTCGGG CTTCTGAAT TCGGTGGCG TCTTCTTCTA CGTCCGTCGA CTGAACAAGA TAAGACTATT CTCAGTCTCC ATTGAGGGGA	AGAAGAAGAT TCTTCTTCTA	GCAGGCAGCT	GAGTTGTTGT CTCAACAACA	ATTCTGATAA TAAGACTATT	GAGTCAGAGG	GAGTCAGAGG TAACTCCCGT CTCAGTCTCC ATTGAGGGCA
1841	TGCGGTGCTG ACGCCACGAC	TOCGETCETE TTAACGGTGG AGGCAGTGT ACTCTGAGGA GTACTCGTTG CTGCCGCGGG CGCCACCAGA CAYAATAGGT ACGCGAGGAC AATTGCCACC TCCCGTCACA TCAGAGTGGT CATGAGGAAC GACGGCGGG GGGGGGTG TATATATGA	AGGCCAGTGT TCCCGTCACA	AGTCTGAGCA TCAGACTCGT	GTACTCGTTG	CTGCCGCGCG	CTGCCGCGCG CGCCACCAGA CATAATAGCT GACGCGCGC GCGCTGGTCT GTATTATCGA	CATAATAGCT
+2								2
1921	GACAGACTAA CTGTCTGATT	GACAGACTAA CAGACTGTTC CTTTCCATGG GTCTTTTCTG CACTCACCGT CGTCCACCTA AGATTCACC ATGCCTGCAT CGTCTCATT TCTCTCACAAG GAAAGGTACC CAGAAAAGAC GTCAGTGGCA GCAGCTGGAT TCTTAAGTGG TACCGACGTA	CTTTCCATGG	GTCTTTTCTG CAGAAAAGAC	CAGTCACCGI CGICGACCIA GICAGIGGCA GCAGCIGGAI	CGTCGACCTA	EcoRI  AGAATTCACC TCTTAAGTGG	ATGGCTGCAT TACCGACGTA
2001	+2 Y A A Q G Y K V L V L N P S V A A T L G F G A Y M S K A A T L G F G A Y M S K I ATCCACCTCA GGCTATAAG GTGCTAGTAC TCAACCCCTC TGTTGCTGA AAACTGGGCT TTGCTGCTA CATCTCAAG TA CATCGAGGT GAACAGGTAG ACAACGAGATGTG	Y A A Q G Y K V L V L N P S V A A T L G F G A Y ANGEGACIA GAGCTATARAG CIGCTACTAC TCAACCCCTC TGTTGCTGCA ACACTGGGCT TTGGTGCTATA TAGGTGGAG ACACGAGGT TGTGACCCGA AACAGGAGAT	V L V L GTGCTAGTAC	N P S TCAACCCTC AGTTGGGGAG	V A A I TGTTGCTGCA A	T L G F	G A Y TTGGTGCTTA AACCACGAAT	M S K CATGTCCAAG GTACAGGTTC

FIG. 3-Page 3

- GGGCAAAGA CGTCCGTTGC GCAGGCAACG 24 CCCGTTTTCT 4 5841
- AAGGGGGTC GTAAGCCAGC TTCCCCCCAG CATTCGGTCG G ტ +5 5921
- R L I TCGTCTCATC AGCAGAGTAG
- S 3 ď 0 > ы Þ ĸ 0 G Д S × 0 1 G X S S Ġ Σ > Ø ы
- GTGGAAGTCC CACCTTCAGG GTTGAATTCC TCGTGCAAGC CAACTTAAGG AGCACGTTCG ECORI ----IGGCGTGAT GGGAAGCTCC TACGGATTCC AATACTCACC AGGACAGCGG ACGGGCACTA CCCTTCGAGG ATGCCTAAGG TTATGACTGG TCCTGTCGCC TGGCCGTGAT
- K K T P M G F S Y D T R C F D S T V T E S D I R T E E AAGAAAACC CAATGGGTT CTCCTATGAT ACCGCTGCT TTGACTCCAC AGTCATTGAG ACCAACCG GTTACGGACT TTCTTTTGGG GTTACCCCAA GAGCATACTA TGGGCGACGA AACTGAGGTG TCACTGACTC TCGCTGTAGG CATGCCTCCT 6161
- V A I K S L T E R L Y V G GTGGCCATCA AGTCCCTCAC CGAGAGGCTT TATGTTGGG CACCGGTAGT TCAGGGATG GCTCTCGGAA ATACAACCC A I Y Q C C D L D P Q A R GGGAAICTAC CAAIGTIGIG ACCICGACCC CCAAGCCCGG O CCGTIAGAIG GTIACAACAC IGGAGCIGGG GGITCGGGCG + 6241
- CGCTCGCCGC ATGACTGTTG ATCGACACCA ပ ~ ĸ × G ပ E N G P L T N S R GCCCTCTTAC CAATTCAAGG GITAAGIICC CGGGAGAATG

721	GCCTGGCATT CGGACCGTAA		ATGCCCAGTA CATGACCTTA TACGGGTCAT GTACTGGAAT	CGGGACTITC	CGGGACTITC CIACTIGGCA GCCCTGAAAG GATGAACCGT		GTACATCTAC GTATTAGTCA TCGCTATTAC CATGTAGATG CATAATCAGT AGCGATAATG	TCGCTATTAC AGCGATAATG
801	CATGGTGAT(	GCCAAAACCG	CATGGTGATG CGGTTTTGGC AGTACACCAA TGGGCGTGGA TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCA GTACCACTAC GCCAAAACCG TCATGTGGTT ACCCGGACCT ATGGCCAAAC TGAGTGCCCC TAAAGGTTCA GAGGTGGGGT	TGGGCGTGGA	TAGCGGTTTG	ACTCACGGGG TGAGTGCCCC	ATTTCCAAGT TAAAGGTTCA	CTCCACCCCA
881	TTGACGTCAA AACTGCAGTI	A TGGGAGTTTG	TIGACCTCAA TOGGAGTITG ITTIGGCACC AAAATCAACG GGACTITCCA AAATGTCCTA ATAACCCCGG CCCGTIGACG AACTGCAGTI ACCTCAAAC AAAACGTIG TITTAGTIGC CCTGAAAGT TITACAGAT TATGGGGCG GGGCAACTGC	AAAATCAACG TTTTAGTTGC	GGACTTTCCA	AAAIGICGTA ATAACCCCGC CCCGITGACG TITACAGGAI TAITGGGGCG GGGCAACTGC	ATAACCCGC TATTGGGGCG	CCCGTTGACG
961	CAAATGGGCG GTTTACCCGC	GTAGGCGTGT CATCCGCACA	GAAATGGGCG GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCG TTTAGTGAAC CGTCAGATCG CCTGGAGACG GTTTACCGCC CATCGGCACA TGCCACCCTC CAGATATATT CGTCTCGAGC AAATCACTTG GCAGTCTAGC GGACCTCTGC	GTCTATATAA	GCAGAGCTCG	TTTAGTGAAC AAATCACTTG	CGTCAGATCG	CCTGGAGACG
1041	CCATCCACGC GGTAGGTGCG	TGTTTTGACC	CCATCCACC TOTITICACC TCCATAGAAG ACACCGGGAC CGATCCAGCC TCCGGGGCCG GGAACGGTGC ATTGGAACGC GGTAGGTGGG ACAAAACTGG AGGTATCTTC TGTGGCCCTG GCTAGGTCGG AGGCGCGGG CGTTGCCAGG TAACCTTGCG	ACACCGGGAC TGTGGCCCTG	CGATCCAGCC GCTAGGTCGG	TCCGCGGCCG	GGAACGGTGC	ATTGGAACGC TAACCTTGCG
1121	GGATTCCCCG CCTAAGGGGC	TGCCAAGAGT ACGGTTCTCA	GGATFOCCCG TGCCAAGAGT GACGTAAGTA CCGCCTATAG ACTCTATAGG CACACCCCTT TGGCTCTTAT GCATGCTATA CCTAAGGGGC ACGGTTCTGA CTGCATTGAT GGGGGATATC TGAGATATC GTGTGGGGAA ACCGAGAATA GCATGCATAT	CCGCCTATAG	ACTCTATAGG TGAGATATCC	CACACCCCTT	TGGCTCTTAT	GCATGCTATA
1201	CTGTTTTGG GACAAAAACC	CTTGGGGCCT	GUCTITITIGG CTIGGGGCCT ATACACCCCC GCTCCTTATG CTATAGGTGA TGGTATAGCT TAGCCTATAG GTGTGGGTTA GACAAAAACC GAACCCCGGA TATGTGGGGG CGAGGAATAC GATATCCACT ACCATATCGA ATGGGATATC CACACCCAAT	GCTCCTTATG	CTATAGGTGA	CTATAGGTGA TGGTATAGCT TAGCCTATAG GATATCCACT ACCATATCGA ATGGGATATC	TAGCCTATAG	GTGTGGGTTA
1281	TTGACCATTA AACTGGTAAT	TTGACCACTC	TICACCATTA TICACCACTC CCCTAITGGT GACGATACTT TCCATTACTA ATCCATAACA TGGCTCTTTG CCACAACTAT AACTGGTAAT AACTGGTGAG GGGATAACCA CTGCTATGAA AGGTAATGAT TAGGTATTGT ACCGAGAAAC GGTGTTGATA	GACGATACIT TCCATTACTA CTGCTATGAA AGGTAATGAT	TCCATTACTA	ATCCATAACA TAGGTATTGT A	TGGCTCTTTG (	CCACAACTAT
1361	CTCTATTGGC GAGATAACCG	TATATGCCAA ATATACGGTT	CICTATIGGC TATATGCCAA TACTCTGTCC TICAGAGACT GACACGGACT CTGTATITIT ACAGGATGGG CTCCATTAT GAGATAACCG ATATACGGTT ATGAGACAGG AGGTCTCTGA CTGTGCCTGA GACATAAAAA TGTCCTACCC CAGGTAAATA	TTCAGAGACT	GACACGGACT CTGTATTTT CTGTGCCTGA GACATAAAAA	CTGTATTTT A	ACAGGAIGGG GICCAITIAI IGICCIACCC CAGGIAAAIA	STCCATTTAT

FIG. 3-Page 2

				•				
-	TCGCGCGTTT AGCGCGCAAA	T CGGTGATGAC A GCCACTACTG	GGTGAAAACC	CGGTCATGAC GGTGAAAACC TCTGACAAT GCAGCTCCCG GCCACTACTG CCACTTTTGG AGACTGTGTA CGTCGAGGGC	GCAGCTCCCG	GAGACGGTCA CTCTGCCAGT	GAGACGGTCA CAGCTIGTCT CTCTGCCAGT GTCGAACAGA	GTAAGCGGAT CATTCGCCTA
81	GCCGGGAGC/ CGGCCCTCG1	GCCGGGAGCA GACAAGCCG TCAGGGCGCG	TCAGGGGGG	GCCGCACCA CACAAGCCC TCAGCGCGC TCAGCGCGT TTGGCGGGTG TCGGGGCTGG CTTAACTATG	TTGGCGGGTG	TCGGGGCTGG	TCAGCGGGG TTGGCGGGTG TCGGGGCTGG CTTAACTATG AGTCGCCCAC AACCGCCCAC AGCCCCGACC GAATTGATAC	CGGCATCAGA
161	GCAGATTGTA	CTGAGAGTGC	A A D T A T A D O A	CCACATTGTA CTCACACTCC ACCATANCAA ACAMPANAMAAA	StuI	H		
1	CGTCTAACAT	GACTCTCACG	TGGTATACTT	CGAAAAACGT	AAAGUUTAGG CCTCCAAAAA TTTCGGATCC GGAGGTTTTT	CCTCCAAAA GGAGGTTTTT	AGCCTCCTCA TCGGAGGAGT	CTACTTCTGG GATGAAGACC
241	AATAGCTCAG TTATCGAGTC	AGGCCGAGGC TCCGGCTCCG	GGCCTCGGCC	AATAGCTCAG AGGCCAGGC GCCTCGGC TCTGCATAA TAAAAAAAT TAGTCAGCCA TGGGGGGGAG AATGGGGGGG TTATGGAGTC TCGGGCTGCG CGGAGCGG AGACGTAITT ATTTITITA ATGAGTGGGT ACGCGGGTO TTACGGGG	TAAAAAAAT ATTTTTTA	TAGTCAGCCA	TGGGGCGGAG	AATGGGCGGA
321	ACTGGGCGGG TGACCCGCCC	GAGGGAATTA	TTGGCTATTG	ACTGGGCGGG GAGGGAATTA TTGGCTATTG GCCATTGCAT ACGTTGTATC TATATCATAA TATGTACATT TATATTGGGT TGACCGGCCC CTCCCTTAAT AACGGATAAC GGTAACGTA TGCAACATAG ATATAGTATT ATACATGTAA ATATAACGA	ACCTIGIAIC TATAICAIAA TGCAACAIAG AIAIAGIAIT	TATATCATAA ATATAGTATT	TATGTACATT TATATTGGCT ATACATGTAA ATATAACGGA	TATATTGGCT
401	CATGTCCAAT	ATGACCGCCA TACTGGCGGT	TGTTGACATT ACAACTGTAA	GATCHCGAAT ATGACCGCCA TCTTGACATT CATTATTGAC TAGTTATTAA TAGTAATCAA TTACGGGGGT GTAGAGGGTTA ATGATTAGTT AATGCCCCAG	TAGTTATTAA	TAGTAATCAA TTACGGGGTC ATCATTAGTT AATGCCCAG	TTACGGGGTC .	ATTAGTTCAT
481	AGCCCATATA TCGGGTATAT	TGGAGTTCCG ACCTCAAGGC	CGTTACATAA	AGCCATATA TGGACTICCG CCTIACATAA CTTACGCTAA ATGGCCGGC TGGCTGACG CCCAACGGC CCCACCGC TGGCTGACG CGCAACTGC CCCAACTATAT ACCGCGGG ACCAACTGG GGGTTGCTAAT GAATGCCATT TACGGGGGGG ACCAACTGG GGGTTGCTAG CAACTGCAACTGC AGGTTTATA CAAACTGGAATGG AGGTTTATA CAAAATGAAA AGGAAAAAAAAAA	ATGGCCCGCC	TGGCTGACCG	CCCAACGACC	CCGCCCATT
561	GACGTCAATA CTGCAGTTAT	ATGACGTATG TTCCCATAGT TACTGCATAC AAGGGTATCA	TTCCCATAGT	ATGACCTATG TICCCATAGT AACGCCAAIA GGGACTTTCC ATTGACGTCA ATGGGTGGAG TATTTACGGT TACTGCATAC AAGGCTATCA TIGGGGTTAT CCCTGAAAGG TAACTGCAGT TACCCACTC ATAAATGCCA	GGGACTTTCC	ATTGACGTCA A	ATGGGTGGAG TATTTACGGT	TATTACGCT
641	AAACTGCCCA TTTGACGGGT	CTTGGCAGTA GAACCGTCAT	CATCAAGTGT GTAGTTCACA	CITGGGGTA CATCAGGG ATCATATGC AGTCGGCC CTATTGAC TCATGACG TAAATGCCC GAACGTCAT GTATTGAA TAGTATAGG TTCAGGGG GAATAATTGA ACTTAGAA ACTTAGAAA ACTTAGAA ACTTAGAAA ACTTAGAAAA ACTTAGAAA ACTTAGAAAAA ACTTAGAAAAA ACTTAGAAAAAAAAAA	AAGTCCGCCC (	CCTATTGACG 2	TCAATGACGG TAAATGGCCC	TAAATGGCCC
							200000000000000000000000000000000000000	9990081111

FIG. 3-Page 1

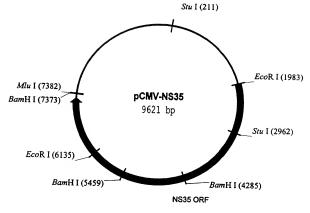


FIG. 2

#### Cloning Scheme for Generating pCMV-NS35

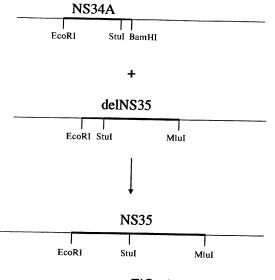


FIG. 1



FIG. 23

5449 APAI,

GlyWalArgAlaThrArgLysThrSerGluArgSerGlnProArgGlyArgArgGlnPro GGTGTGGCGCGCGAGAGAAGACTTCCGAGCGGTCGCAACCTCGAGGTAGACGTCAGCCT CCACACCCGCGTGCTCTTTCTGAAGGCTCGCAGCGTTGGAGCTCCATTCGAGTCGA

5467 BSSH2, 5478 XMNI, 5502 XHOI, 5511 AAT2,

11eProLysAlaArgArgProGluGlyArgThrTrpAlaGlnProGlyTyrProTrpPro ATCCCAAGGCTCGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACCCTTGGCCC TAGGGTTCCGAGCAGCCGGGCTCCCGTCCTGGACCCGAGTCGGGCCCATGGAACCGG TAGGGTTCCGAGCAGCCGGGCTCCCGTCCTGGACCCGAGTCGGGCCCATGGAACCGG

5548 ALWN1, 5558 ESP1, 5564 SMAI XMAI, 5568 KPNI,

LeuTyrGlyAsnGluGlyCysGlyTrpAlaGlyTrpLeuLeuSerFroArgGlySerArg
CTCTATGGCAATGAGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCGTGGCTCTCGG
GAGATACCGTTACTCCGAGGCCCACCGCGCCTACCGAGAGGGAAAGGGGCACGAGAGGC

ProSerTipGlyProThrAspProArgArgArgArgArgAsnLeuGlyLysvallleAsp
5642 CTAGCTGGGGCCCCACGACCCCGGCGTAGGTCGGCGATTTGGGTAAGGTCATCGAT
GGATCGACCCCGGGGTGTCTGGGGGCCGCATCCAGCGCGTTAAACCCATTCCAGTAGCTA

5650 APAI, 5696 CLAI,

ThrLeuThrCysGlyPheAlaAspLeuMetGlyTyrIleProLeuValGlyAlaProLeu
ACCCTTACGTGCGCTTCGCCGACCTCTT
TGGGAATGCACCCGAAGCGGCTGGAGTACCCATGTTGTGGAACTGCCGGGGGAGA
TGGAATGCACCCGAAGCGGCTGGAGTACCCATGTATGCGAACGAGCAGCCGGGGGAGA

5724 HGIE2, 5750 KAS1 NARI, 5756 ECON1,

GlyGlyAlaAlaArgAlaOC AM 5762 GGAGGCGCTGCCAGGGCCTAATAGTCGAC CCTCCGCGACGGTCCCGGATTATCAGCTG

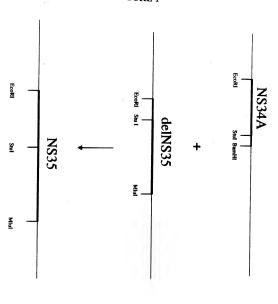
5785 SALI.

FIG. 22-Page 10



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APPL PARTS	NPL	CTNF
NOTES AND AND ASSESSMENT OF THE PARTY OF THE	Non-Patent Literature	Count Non-Final
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Internal Misc. Pape	Oath or Declaration	Count Restriction
Section 15 Section 1	Petition PET.	EXIN
Mise incoming Letter	Petition	Examiner Interview
371P	RETMAIL	MQO3
PCT Papers in a 371Application	Mail Returned by USPS	DO/EO Acceptance
Amendment Including Elections	SEQLIST	M905
	Sequence Listing	DO/EO Missing Requirement
ABST	Specification SPEC	
Abstract	Specification	NFDR Formal Drawing Required
ADS	SPEC NO	
Application Data Sheet	Specification Not in English	NOA
AF/D	TRNA Transmittal New Application	PETDEC
Affidavit or Exhibit Received	Transmittal New Application	Petition Decision
APPENDIX		
Appendix		
ARTIFACT	OUTGOING	INCOMING
Artifact		INCOMING
BIB	A CIMS	AP.B
Bib Data Sheet	MISC/Office Actions	Appeal Brief
CLM	1449	C.AD
Claim	Signed 1449	C.AD Change of Address
COMPUTER	892	N/AD
Computer Program Listing	892	Notice of Appeal
CRFL	ABN	
All CRF Papers for Backfile	Abandonment	PA Change in Power of Attorney
DIST	APDEC	
Terminal Disclaimer Filed	APDEC Board of Appeals Decision	Applicant Remarks in Amendment
_ DRW /U	APEA	
Drawings	Examiner Answer	Extension of Time filed separate
FOR '	CTAV	entonois of time med separate
Foreign Reference	CTAV	
FRPR	CTEO	
Foreign Priority Papers	Count Ex parte Quayle	
IDS	CTFR	
IDS Including 1449	Count Final Rejection	File Wrapper
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Internal	ECBOX	FWCLM
	Evidence Copy Box Identification	File Wrapper Claim
SRNT	WCLM	IIFW
Examiner Search Notes	Claim Worksheet	IIFW
CLMPTO	Fee Worksheet WFEE	ODEW
PTO Prepared Complete Claim Set	Fee Worksheet	File Wrapper Search Info



NO MARINED

Cloning Scheme for Generating pCMV-NS35